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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 16:52:01 ; Search time 4299 Seconds
(without alignments)
2530.037 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 230
Sequence: 1 MASLGLQVYLIGLGLG.....PQGPVKSEFNSYSUTGV 230

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9045947

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-UNITS-bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdt -LIST=45
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
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-Fgapext=7 -Ygapop=60 -Ygapext=60 -Delop=6 -Delext=7

Database :

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4: gb_cm: *
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6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sce: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	100.0	693	6	CQ732222 Sequence
2	230	100.0	693	2	AF250558 Homo sapi
3	230	100.0	1400	6	AR340765 Sequence
4	230	100.0	1400	6	BD085944 Elongatio

5	230	100.0	1475	6	AX092348 Sequence
6	230	100.0	1475	6	AX299996 Sequence
7	230	100.0	1475	6	AX395213 Sequence
8	230	100.0	1475	6	AX454606 Sequence
9	230	100.0	1475	6	AX464358 Sequence
10	230	100.0	1475	6	AX491084 Sequence
11	230	100.0	1475	6	AX697065 Sequence
12	230	100.0	1475	6	AX584474 Homo sapi
13	230	100.0	1506	9	BC014424 Homo sapi
14	230	100.0	1518	9	BC071747 Homo sapi
15	230	100.0	1918	9	AF177340 Homo sapi
16	230	100.0	2742	6	BD237562 Membrane-
17	230	100.0	2863	6	AX136129 Sequence
18	230	100.0	2863	6	BD123517 Secretory
19	230	100.0	2863	9	AK075371 Homo sapi
20	230	100.0	2959	9	AK075405 Homo sapi
21	230	100.0	109465	9	AL158821 Human DNA
22	186	80.9	1441	6	AX286822 Sequence
23	131	57.0	693	6	AX497200 Sequence
24	127	55.2	1524	6	AR340718 Sequence
25	127	55.2	1524	6	BD085897 Elongatio
26	67	29.1	615	6	AX136475 Sequence
27	67	29.1	615	6	BD123715 Secretory
28	59	25.7	1032	4	AB115779 Bos tauri
29	58	25.2	779	6	AX286824 Sequence
30	58	25.2	791	6	E31591 Tight junct
31	58	25.2	791	10	AF072128 Mus muscu
32	58	25.2	953	4	AF358907 Canis fam
33	58	25.2	2828	10	BC015252 Mus muscu
34	58	25.2	184872	10	AL672243 Mouse DNA
35	58	25.2	239385	2	AC109686 Rattus no
36	58	25.2	250600	2	AC136646 Rattus no
37	58	25.2	268828	2	AC091513 Rattus no
38	56	24.3	405	6	AX939252 Sequence
39	56	24.3	405	6	BD077679 5'EST of
40	55	23.9	324	6	AX939253 Sequence
41	55	23.9	324	6	BD077680 5'EST of
42	47	20.4	300	6	BD212444 Novel hum
43	36	15.7	182	6	AK072760 Sequence
44	31	13.5	49323	2	AC107455 Mus muscu
45	16	7.0	51	6	AX165469 Sequence

ALIGNMENTS

RESULT 1	CQ732222	693 bp	DNA	linear	PAT 03-FGB-2004
LOCUS	Sequence 18156 from Patent WO02068579.				
DEFINITION	CQ732222				
ACCESSION	CQ732222.1	GI:42311107			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.				
JOURNAL	Kits, such as nucleic acid arrays, comprising a majority of				
FEATURES	humanexons or transcripts, for detecting expression and other uses				
source	thereof Patent: WO 02068579-A 18156 06-SEP-2002;				
	PE Corporation Location/Qualifiers				
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	/db_xref="taxon:9606"				

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Pred. No.: 230.00 Matches: 230

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 6
 Gaps: 0

US-09-787-677a-3 (1-230) x CQ732222 (1-693)

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 Db 1 ATGGCCCTCTTGCCCTCCAACTTGCGGCTACATCTAGGCCCTTCTGGGGCTTTGGGC 60
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrrpIysThrSerSerTyrValIGlyAlaSerIle 40
 Db 61 ACACGTGGTCCCATGCTGCTCCAGCTGGAAACAAATCTTATGTCGGTCCAGCAT 120
 QY 41 ValThrAlaValIGlyPheSerIysGlyLeuTrrpMetGluCysAlaThrHisSerThrGly 60
 Db 121 GTGACAGCATGTGGCTTCTCCAGGGCTCTGGATGGAAATGGCACACACAGCAGGC 180
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
 Db 181 ATCAACCCAGTGTACATCTATAGCACCTTCTGGGCTCTGCCCTGACATCCAGGCTGCC 240
 QY 81 GlnAlaMetMetValIThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 241 CAGGCCATGATGTGATCATCATCAGTCAATCTCTCCCTGGGCTGCATTAATCTGTGGTG 300
 QY 101 GlyMetArgCysThrValIlePheCysGlnGlnSerArgAlaIysAspArgValAlaVal 120
 Db 301 GGCGATGATGACACAGTCTTCTCCAGGAATCCGACCAAGACAGATGGCGGTAGCA 360
 QY 121 GlyGlyValPhePheIleLeuGlyGlyIleLeuGlyIlePheIleProValAlaTrrpAsnLeu 140
 Db 361 GGATGAGCTTTTTCATCTTGGAGGCTCTCTGGGATTCATCTCTGTGCTGGAACTT 420
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValIProAspSerMetIysPheGlnIle 160
 Db 421 CATGGGATCTTACCGGAGCTTCTACTCACACTGGTGCCTGACAGCATGAATTTGAAATT 480
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 Db 481 GGAGAGGCTCTTACTTGGGATTAATTTCTTCTCTGTTCTCCGATGAGCTGGAAATATC 540
 QY 181 LeuCysPheSerCysSerSerGlnArgAspArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 541 CTCTGCTTTTCCGCTCATCTCCAGAAATCGCTCCAACTACATGATGCTTACCAAGCC 600
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValIlysSerGlu 220
 Db 601 CAACCTCTTCCCAAGAGACTCTCCAAAGGCTGTCAACTCCCAAGTCAAGAGTGAAG 660
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 661 TTCAATTCCTACAGCTGACAGGATATGTG 690

RESULT 2
 AF250558 693 bp mRNA linear PRI 10-JUN-2002
 LOCUS Homo sapiens claudin-2 mRNA, complete cds.
 DEFINITION AF250558
 VERSION AF250558.1 GI:9755008
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Chordata; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Sakaguchi, T., Gu, X., Golden, H.M., Suh, E., Rhoads, D.B. and
 Reinacker, H.C.
 Cloning of the human claudin-2 5'-flanking region revealed a
 TATA-less promoter with conserved binding sites in mouse and human
 for caudal-related homeodomain proteins and hepatocyte nuclear
 factor-1alpha

JOURNAL J. Biol. Chem. 277 (24), 21361-21370 (2002)
 MEDLINE 22050612
 PUBMED 11934881
 REFERENCE 2 (pages 1 to 693)
 AUTHORS Reinacker, H.-C., Sakaguchi, T. and Golden, H.M.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAR-2000) Gastrointestinal Unit, Massachusetts
 General Hospital, Fruit Street, Boston, MA 02114, USA
 FEATURES
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ORIGIN

Alignment Scores:

Pred. No.: 2,126-238 Length: 693
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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-787-677a-3 (1-230) x AF250558 (1-693)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValIGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
 Db 1 ATGGCCCTCTTGCCCTCCAACTTGCGGCTACATCTAGGCCCTTCTGGGGCTTTGGGC 60
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrrpIysThrSerSerTyrValIGlyAlaSerIle 40
 Db 61 ACACGTGGTCCCATGCTGCTCCAGCTGGAAACAAATCTTATGTCGGTCCAGCAT 120
 QY 41 ValThrAlaValIGlyPheSerIysGlyLeuTrrpMetGluCysAlaThrHisSerThrGly 60
 Db 121 GTGACAGCATGTGGCTTCTCCAGGGCTCTGGATGGAAATGGCACACACAGCAGGC 180
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
 Db 181 ATCAACCCAGTGTACATCTATAGCACCTTCTGGGCTCTGCCCTGACATCCAGGCTGCC 240
 QY 81 GlnAlaMetMetValIThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 241 CAGGCCATGATGTGATCATCATCAGTCAATCTCTCCCTGGGCTGCATTAATCTGTGGTG 300
 QY 101 GlyMetArgCysThrValIlePheCysGlnGlnSerArgAlaIysAspArgValAlaVal 120
 Db 301 GGCGATGATGACACAGTCTTCTCCAGGAATCCGACCAAGACAGATGGCGGTAGCA 360
 QY 121 GlyGlyValPhePheIleLeuGlyGlyIleLeuGlyIlePheIleProValAlaTrrpAsnLeu 140
 Db 361 GGATGAGCTTTTTCATCTTGGAGGCTCTCTGGGATTCATCTCTGTGCTGGAAATCTT 420
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValIProAspSerMetIysPheGlnIle 160
 Db 421 CATGGGATCTTACCGGAGCTTCTACTCACACTGGTGCCTGACAGCATGAATTTGAAATT 480
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180

Db 481 GGAGAGCTCTTACTGGGCGATTATTTCTCCCTGTTCCCTCGAAGCTGGAATATC 540
Qy 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 541 CTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCAACTACTACATGCTTACCAAGCC 600
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysVallySerGlu 220
Db 601 CAACCTCTTCCCAAGAGCTCTCCAGGCTGTCAACCTCCCAAGTCAGAGTAGAG 660
Qy 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 661 TTCAATTCTTACAGCTGACAGGATATGTG 690
RESULT 3
AR340765 1400 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 139 from patent US 6573068.
DEFINITION AR340765
ACCESSION AR340765 GI:33732507
VERSION AR340765.1 GI:33732507
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1400)
AUTHORS Milne Edwards,V.-B.D., Duclert,A. and Bougueleret,L.
TITLE Claudin-50 protein
JOURNAL Patent: US 6573068-A 139 03-JUN-2003;
FEATURES
source location/Qualifiers
1..1400
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Pred. No.: 4,34e-238 Length: 1400
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
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Qy 21 ThrLeuValAlaMetLeuLeuProSerTTrpLysThrSerSerTyrValGlyAlaSerIle 40
Db 96 ACACGTGTTCCAGTGCCTCCCGACGTGAAAAACAATTCTTATGTCGGGCGCAGCAT 155
Qy 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
Db 156 GTGACACAGTTGGCTTCTCCAGGGCTCTGGAGTGAATGTGCACACACAGACAGGC 215
Qy 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
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Db 336 GGCATGAGATGACAGCTTCTGCGCAGGAATCCGAGCCAAAGACAGAGTGGCGGTGCA 395
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
Db 396 GGTGAGCTCTTTTCACTCTTGAAGGCTCTCTGGGATTCATCTCTGTTGGCTGGAATCTT 455

Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
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Qy 161 GlyValAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 516 GGAGAGCTCTTACTTGGGCGATTATTTCTCCCTGTTCCCTGATAGCTGAAATCATC 575
Qy 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 576 CTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCAACTACTACATGCTTACCAAGCC 635
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysVallySerGlu 220
Db 636 CAACCTCTTCCCAAGAGCTCTCCAGGCTGTCAACCTCCCAAGTCAGAGTAGAG 695
Qy 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 696 TTCAATTCTTACAGCTGACAGGATATGTG 725
RESULT 4
BD085944 1400 bp DNA linear PAT 27-AUG-2002
LOCUS Elongation CDNA of secretory protein.
DEFINITION BD085944
ACCESSION BD085944
VERSION BD085944.1 GI:22631554
KEYWORDS JP 2001523453-A/86.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1400)
AUTHORS Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
TITLE Elongation CDNA of secretory protein
JOURNAL Patent: JP 2001523453-A 86 27-NOV-2001;
GENSET
OS Homo sapiens (human)
PN JP 2001523453-A/86
PD 27-NOV-2001
PR 13-NOV-1998 JP 2000521191
PR 13-NOV-1997 US 60/066677,17-DEC-1997 US 60/069957 PR
09-FEB-1998 US 60/074121,13-APR-1998 US 60/081563 PR
10-AUG-1998 US 60/096116,04-SEP-1998 US 60/099273 PI LYDIE
BOUGUELERET,AYMERIC DUCLEERT,JEAN BAPTISTE DOMAS MILNE PI EDWARDS
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
C12N1/21,
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Von Heijne matrix
CC score 5.68999980926514
CC seq ILGLDLGLTLVA/ML
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Alignment Scores:
Pred. No.: 4,34e-238 Length: 1400
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20

Db 36 ATGGCTCTCTTGGCTCCAACTTGAGGCTACACTTACGCTTCTGGGCTTTGGGC 95
 Qy 21 ThrleuValAlaMetleuLeuProSerTrpLysThrSerSerTrpValAlaSerIle 40
 Db 96 ACACGTGGTGGCAGCTGCTCCAGCTGGAACCAAGTTCTTATGCGGAGCAGCAT 155
 Qy 41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
 Db 156 GTGACACAGTGGCTTCTCCAAAGGCTCTGAGTGAATGTCCACACACAGCAGCAGC 215
 Qy 61 IleThrGlnCysAspIleTrpSerThrleuGlyLeuProAlaAspIleGlnAla 80
 Db 216 ATCACCCAGTGTGACATCTATAGCACTTCTGGGCTGCGCCGTGACATCAGAGCTGCC 275
 Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerleuAlaCysIleIleSerVal 100
 Db 276 CAGGCCATGATGGAGACATCCAGTCAATCTCTCCCTGCGCTCATTAATCTGTGTG 335
 Qy 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAla 120
 Db 336 GGCATGAGATGCACAGTCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGTAGCA 395
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 Db 396 GGTGAGCTCTTTTCATCTTGAGGCTCTGAGGATTCATCTGTTGCTGGAACTCT 455
 Qy 141 HisGlyIleLeuArgAspPheTrpSerProleuValProAspSerMetLysPheGluIle 160
 Db 456 CATGGAGATCTTACGAGACTTCTACTCACCTGAGCTGACACAGCAATGAAATTTGAGATT 515
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 Db 576 CTCTGCTTTCT 635
 Qy 201 GlnProleuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
 Db 636 CAACCTCTTGCACAGAGGCTCTCCAGGCTGTCACTCCCAAGCAAGAGTAG 695
 Qy 221 PheAsnSerTrpSerLeuThrGlyTrpVal 230
 Db 696 TTCAATTCCTACAGCTGACAGGATGTG 725
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 AX092348 1475 bp DNA linear PAT 21-MAR-2001
 LOCUS Sequence 79 from Patent WO0116318.
 DEFINITION AX092348
 ACCESSION AX092348
 VERSION AX092348.1 GI:13444488
 KEYWORDS
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Baton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
 Wood,W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0116318-A 79 08-MAR-2001;
 Genentech, Inc. (US)
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 ORIGIN
 Alignment Scores:

Pred. No.: 4,57e-238 Length: 1475
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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 US-09-787-677a-3 (1-230) x AX092348 (1-1475)
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 Qy 21 ThrleuValAlaMetleuLeuProSerTrpLysThrSerSerTrpValAlaSerIle 40
 Db 182 ACACGTGGTGGCAGCTGCTCCAGCTGGAACCAAGTTCTTATGCGGAGCAGCAT 241
 Qy 41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
 Db 242 GTGACACAGTGGCTTCTCCAAAGGCTCTGAGTGAATGTCCACACACAGCAGCAGC 301
 Qy 61 IleThrGlnCysAspIleTrpSerThrleuGlyLeuProAlaAspIleGlnAla 80
 Db 302 ATCACCCAGTGTGACATCTATAGCACTTCTGGGCTGCGCCGTGACATCAGAGCTGCC 361
 Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerleuAlaCysIleIleSerVal 100
 Db 362 CAGGCCATGATGGAGACATCCAGTCAATCTCTCCCTGCGCTCATTAATCTGTGTG 421
 Qy 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAla 120
 Db 422 GGCATGAGATGCACAGTCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGTAGCA 481
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 Db 542 CATGGAGATCTTACGAGACTTCTACTCACCTGAGCTGACACAGCAATGAAATTTGAGATT 601
 Qy 161 GlyIleAlaLeuTrpLeuGlyIleIleSerSerleuPheSerleuIleAlaGlyIle 180
 Db 602 GGAAGAGCTCTTTCATCTGCGCATTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 661
 Qy 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerSerTrpTrpAspAlaTrpGlnAla 200
 Db 662 CTCTGCTTTCT 721
 Qy 201 GlnProleuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
 Db 722 CAACCTCTTGCACAGAGGCTCTCCAGGCTGTCACTCCCAAGCAAGAGTAG 781
 Qy 221 PheAsnSerTrpSerLeuThrGlyTrpVal 230
 Db 782 TTCAATTCCTACAGCTGACAGGATGTG 811
 RESULT 6
 AX299996 1475 bp DNA linear PAT 26-NOV-2001
 LOCUS Sequence 1 from Patent WO0166740.
 DEFINITION AX299996
 ACCESSION AX299996
 VERSION AX299996.1 GI:17129473
 KEYWORDS
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Baton,D.L., Fung,S., Goddard,A., Godowski,P.J., Grimaldi,C.J.,
 Gurney,A.L., Tumas,D., Watanabe,C.K., Wood,W.I. and Zhang,Z.
 TITLE Compositions and methods for the treatment of immune related
 diseases

JOURNAL Patent: WO 0166740-A 1 13-SEP-2001;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
Source 1.1475
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Pred. No.: 4.57e-238 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-787-677a-3 (1-230) x AX299996 (1-1475)

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Db 122 ATGGCCCTCTTGGCTCCCACTTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerSerTyrValGlyAlaSerIle 40
Db 182 ACACGTGTTCCATGCTGCTCCCACTGAGAAACAAGTTCTTATGTCGGTGCACGATT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
Db 242 GTACAGACAGATGGCTTCTCCAGAGGCTCTGATGATGATGTCACACACAGCAGAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCAGATGATGATCATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 362 CAGGCCATGATGATGATCATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
Db 422 GGCATGATGATGATGATCATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 481
QY 121 GlyGlyValPhePheIleLeuGlyIleLeuLeuGlyPheIleProValAlaIlePheLeu 140
Db 482 GGTGAGATCTTTTCACTCTTGAGGCTCTCTGGGATTCATCTCTGCTGGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 542 CATGGATCTTACGGGACTTCTACTCACCTGATGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GAGAGGCTCTTACTTGGGACTTATTTCTTCCCTGTTCTCCGATAGTGGGAAATCATC 661
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCTCGCTCATCCAGAGAAATGCTCCAACTACTACATGATGCTCAAGACC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlyValIleValSerGlu 220
Db 722 CAACCTTTTCCACAGAGAGCTCTCCAGAGGCTGTCAACCTCCCAAGTCAAGAGTGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCATATCTTACAGCTGACAGGGTATGTG 811

RESULT 7
AX395213 1475 bp DNA linear PAT 18-MAY-2002
LOCUS Sequence 1 from Patent WO0216429.
DEFINITION AX395213
ACCESSION AX395213.1 GI:21066244
VERSION

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Goddard, A., Goddard, P.J., Gurney, A.L., Hillan, K.J., Polakis, P., Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.
TITLE Compositions and methods for the diagnosis and treatment of tumor
JOURNAL Patent: WO 0216429-A 1 28-FEB-2002;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
Source 1.1475
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 4.57e-238 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-787-677a-3 (1-230) x AX395213 (1-1475)

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Db 122 ATGGCCCTCTTGGCTCCCACTTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerSerTyrValGlyAlaSerIle 40
Db 182 ACACGTGTTCCATGCTGCTCCCACTGAGAAACAAGTTCTTATGTCGGTGCACGATT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
Db 242 GTACAGACAGATGGCTTCTCCAGAGGCTCTGATGATGATGTCACACACAGCAGAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCAGATGATGATCATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 362 CAGGCCATGATGATGATCATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
Db 422 GGCATGATGATGATGATCATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 481
QY 121 GlyGlyValPhePheIleLeuGlyIleLeuLeuGlyPheIleProValAlaIlePheLeu 140
Db 482 GGTGAGATCTTTTCACTCTTGAGGCTCTCTGGGATTCATCTCTGCTGGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 542 CATGGATCTTACGGGACTTCTACTCACCTGATGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GAGAGGCTCTTACTTGGGACTTATTTCTTCCCTGTTCTCCGATAGTGGGAAATCATC 661
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCTCGCTCATCCAGAGAAATGCTCCAACTACTACATGATGCTCAAGACC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlyValIleValSerGlu 220
Db 722 CAACCTTTTCCACAGAGAGCTCTCCAGAGGCTGTCAACCTCCCAAGTCAAGAGTGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230

Db 782 TTCATTCTACAGCTGACAGGGTATGTG 811

|||||

RESULT 8
AX454606 1475 bp DNA linear PAT 06-JUN-2002
Sequence 191 from Patent WO0208284.
AX454606
VERSION AX454606.1 GI:21713927

SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerltzen, M.E., Goddard, A.,
Goddard, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Pooni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0208284-A 191 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerltzen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)
; Pooni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.: 4.57e-238 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-787-677A-3 (1-230) x AX454606 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTlleLeuGlyLeuLeuGly 20
Db 122 ATGGCCCTCTTGGCTTCCCACTGTGGCTACATCTTGGGCTTTGGGC 181

QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerTyrValAlaSerIle 40
Db 182 ACATGTTGGCTTGGCTTCCCACTGTGGGAAACAACTTATGTCGGTCCAGCAT 241

QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrPheGlyCysAlaThrHisSerThrGly 60
Db 242 GTGACACAGTTGGCTTCCCAAGGGCTCTGATGAAATGGCACACACAGCAGGC 301

QY 61 TleThrGlnCysAapIleTyrSerThrLeuLeuGlyLeuProAlaAapIleGlnAla 80
Db 302 ATCAACCCAGTGTGATCTATAGCACCTTCTGGGCTGCGCTGATCATCCAGGCTGCC 361

QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGTGACATCCAGTGCAATCTCTCCCTGGGCTGATTAATCTGTGGTG 421

QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaValAaPArGValAlaValAla 120
Db 422 GGCATGAGATGACACAGTCTTGTGCCAAGAAATCCGAGCAAAAGACAGTGGCGTGCA 481

QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrPheLeu 140
Db 482 GGTGGAGTCTTTTTCATCTCTGGAGGCTCTGGGATTCATCTGTGGCTGGAATCTT 541

QY 141 HisGlyIleLeuArgAapPheTyrSerProLeuValProAapSerMetLysPheGluIle 160
Db 542 CATGGATCTCTACGGAGCTTCTACTCACCACTGTGCTACAGCAAGAAATTTGAGATT 601

QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
Db 602 GGAAGAGCTCTTACTTGGGCAATTAATTTCTCCCTGTTCTCCCTGATAGCTGGATCATC 661

QY 181 LeuCyPheSerCysSerSerGlnArgAaArgSerArgTyrTyrAaPAlaTyrGlnAla 200
Db 662 CTGTGCTTTCTGCTCATCCAGAAATCGCTCCAACTACATGATGCTTCCAAAGCC 721

QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValIlysSerGlu 220
Db 722 CAACCTTTGCCACAGAGACTCTCCAGGCTGTGTCAACTCCCAAGTCAGAGTGTG 781

QY 221 PheAaSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCATTCTACAGCTGACAGGGTATGTG 811

RESULT 9
AX464358 1475 bp DNA linear PAT 16-JUN-2002
Sequence 491 from Patent WO0140466.
AX464358
VERSION AX464358.1 GI:21899195

SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Geo, W.Q., Gerltzen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tuma, D., Watanabe, C.K.,
Wood, W.I. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
same
Patent: WO 0140466-A 491 07-JUN-2001;
Genentech Inc. (US)

FEATURES
source 1. 1475
/organism="Homo sapiens"
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ORIGIN

Alignment Scores:
Pred. No.: 4.57e-238 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-787-677A-3 (1-230) x AX464358 (1-1475)

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QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrPheGlyCysAlaThrHisSerThrGly 60
Db 242 GTGACACAGTTGGCTTCCCAAGGGCTCTGATGAAATGGCACACACAGCAGGC 301

QY 61 TleThrGlnCysAapIleTyrSerThrLeuLeuGlyLeuProAlaAapIleGlnAla 80
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Qy	41	ValThrAlaValAlGlyPheSerTyGlyLeuTrpMetGluCysAlaThrHisSerThrGly	60
Db	242	GTGACAGCAGTGGCTTCTCCAAAGGGCTCTGGATGTGAATGTGCAACACAGCAGCAGGC	301
Qy	61	IlleThrGlnCysAspIleTyYrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla	80
Db	302	ATCCACCAAGTGTACATCTATAGCAACCTTCCTGGGCTGGCCCGCTGACATCCAGGCTGCC	361
Qy	81	GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysAlleIleSerValIVal	100
Db	362	CAGGCCATGATGTGATGATCATTCAGAGCAATCTCTCTCCGTGGCTCATTTATCTCTGTGTG	421
Qy	101	GlyMetArgCysThrValAlaPheCysGlnGlnIleSerArgAlaIleAspArgValAlaValAla	120
Db	422	GGCATGATGATGCAACAGTCTTCTGCGCAGAAATCCGAGCAACAAAGACAGATGGCGGTGACA	481
Qy	121	GlyGlyValAlaPhePheIleLeuGlyGlyLeuLeuGlyGlyPheIleProValAlaATPAsnLeu	140
Db	482	GGTGGAGTCTTTTTCATCCCTTGGAGGGCTCTGGGATTCATTCCTGTGGCTGGAAATCTT	541
Qy	141	HisGlyIleLeuArgAspPheTyYrSerSerProLeuValProAspSerMetLysPheGluIle	160
Db	542	CATGGGATCTCTACGGGACTTCTACTCCACATGATGCTGACAGACATGMAATTTGAATTT	601
Qy	161	GlyGlnAlaLeuTyYrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle	180
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Qy	181	LeuCySphSerSerCysSerSerGlnArgAsnArgSerSerTyYrAspAlaTyGlnAla	200
Db	662	CTGCTCTTTCCTGCTCATCCCAAGAAATCGCTCCCAACTGACATGATGCTTACCAAGCC	721
Qy	201	GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValIlySerSerGlu	220
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Qy	221	PheAsnSerTyYrSerLeuThrGlyTyYrVal	230
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ACCESSION	AK697065		
VERSION	AK697065.1	GI:29498042	
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ORGANISM			
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	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE			
AUTHORS	1		
	Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,		
	Bacon,D.L., Gao,W.Q., Pan,J., Botsstein,D., Fong,S., Goddard,A.,		
	Gidowski,P.J., Gurney,A.L., Smith,V., Tunes,D., Wood,W.I.,		
	Goldwaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.		
	Secreted and transmembrane polypeptides and nucleic acids encoding		
	the same		
	Patent: WO 0078961-A 133 28-DEC-2000;		
JOURNAL			
	Genentech Inc. (US)		
FEATURES			
source	Location/Qualifiers		
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ORIGIN			
	Alignment Scores:		

Pred. No.: 4,576-238 Length: 1475
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-787-677a-3 (1-230) x AK697065 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
 Db 122 ATGGCTCTCTTGGCTTCCAACTGTGGGCTACATCTCAGGCTTCTGGGGCTTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLeuThrSerSerTyrValGlyAlaSerIle 40
 Db 182 ACATGGTGTCCAGAGCTGCTCCAGCTGGAACCAAGTCTTAATGTGGTCCAGCAT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
 Db 242 GTGACAGAGTTGGCTTCTCCAAAGGCTCTGATGGAATGTCCACACACAGCAGCGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
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 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValAla 100
 Db 362 CAGGCCATGATGGAGACATCCAGTGCATCTCTCCCTGGGCTGCTGATTAATCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGlnSerAlaValAlaValAspArgValAlaValAla 120
 Db 422 GGCAATGATGACACAGCTTCTTGGCAGGAATCCGAGCCAAAGACAGAGTGGCGGTGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyIleLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
 Db 482 GGTGAGTCTTTTCATCTCTGGAGGCTCTCCGGATTCATCTCTGTTGCTCGAATCTT 541
 QY 141 HisGlyIleLeuAsgAspPheTyrSerProLeuValProAspSerMetLeuPheGlnIle 160
 Db 542 CATGGATCTTACGGAGCTTCTTACTCACCTGAGTGTGCTGACAGATGAATTTGAGATT 601
 QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 Db 602 GGAAGGCTTTTACTTGGCATTAATTTCTCCGTTCTCCCTGATGATCGAATATCTC 661
 QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 662 CTCTGCTTTTCTCTCTCATCCAGGAATGCTCCAACTACTACGATGCTTACCAAGCC 721
 QY 201 GlnProLeuAlaTrpArgSerSerProArgProGlyGlnProPolysValIleSerGly 220
 Db 722 CAACTCTTCCCAAGAGCTCTCCAAAGGCTGTCACTCCCAAGTCAAGAGTAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 782 TTCAATCTCTACAGCTGACAGGATGTG 811

RESULT 12
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 LOCUS Homo sapiens clone DNA64886 claudin-2 (UNQ705) mRNA, complete cds.
 DEFINITION AY358474
 ACCESSION AY358474
 VERSION AY358474.1 GI:37182070
 KEYWORDS FLI_CDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Carnifera; Mammalia; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 1475)
 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E., Heidens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,

Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seeshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagstad,A., Vandlen,R., Watanabe,C., Weiland,D., Woods,K., Xie,M.H., Yamasaki,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
 Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL 12975309
 PUBMED 2 (bases 1 to 1475)
 REFERENCE Clark,H.F.
 AUTHORS Direct Submission
 TITLE Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
 JOURNAL Location/Qualifiers

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 SEFNSVSLGVV"

ORIGIN
 Alignment Scores:
 Pred. No.: 4,576-238 Length: 1475
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-787-677a-3 (1-230) x AY358474 (1-1475)

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 Db 302 ATCACCCAGTGTGACATCTATAGCACCTTCTGGGCTCTGCCGCTGACATCAGGCTGCC 361
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 Db 422 GGCAATGATGACACAGCTTCTTGGCAGGAATCCGAGCCAAAGACAGAGTGGCGGTGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyIleLeuLeuGlyPheIleProValAlaTrpAsnLeu 140

Db 422 GGATGATGATGACAGCTCTTCTGCCAGATATCCGACCAAGACAGAGTGGCGGTAGCA 481
Qy 121 G1G1G1ValPhePhe11LeuG1G1LeuLeuG1Phe11LeuProVal1Ala1TrpAsnLeu 140
Db 482 GGTGAGCTTTTTCATCTCTTGAGGCTCTGCGATTCATCTCGTGGCTGGATCTT 541
Qy 141 H1G1G1LeuAlaGAspPheTyrSerProLeuVal1ProAspSerMetLeuPheGlu11Le 160
Db 542 CATGGATCTTACGGAGCTTCTACTCACCAGCTGAGCTGCTGACAGCATTAATTTGAGATT 601
Qy 161 G1G1Ala1LeuTyrLeuG1G1Le11LeSerSerLeuPheSerLeu11AlaG1G1Le11Le 180
Db 602 GGAGAGGCTTTTACTTCTTGGCATTTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATC 661
Qy 181 LeuCyPheSerCySerSerSerG1AlaGAsnAlaGSerSer1TyrTyrAla1AlaTyrG1Ala 200
Db 662 CTCTGCTTTTCTGCTCTACCCAGAAATGCTTCCAACTACTAGATGCTTACCAACCC 721
Qy 201 G1AlaProLeuAla1ThAlaSerSerProAlaGProG1G1AlaProProG1Val1LeuSerG1u 220
Db 722 CAACCTCTTGGCACAAGAGCTCTCCAAAGGCTGTCAACTCCCAAGTCAAGAGTANG 781
Qy 221 PheAsnSerTyrSerLeuThrG1G1TyrVal 230
Db 782 TTCAATCTCTACAGCTGACAGGATATGTG 811

RESULT 14
BC071747 1618 bp. mRNA linear PRI 25-JUN-2004
LOCUS Homo sapiens claudin 2, mRNA (CDNA clone MGC:88250 IMAGE:30322852),
DEFINITION complete cds.
ACCESSION BC071747
VERSION BC071747.1 GI:47938251
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1618)
Strauberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmer,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Dichenko,L., Marsina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Seipleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schneitz,T.E., Brownstein,M.J., Uedin,T.B., Tothliki,S.,
Carninci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,K.D., Mullahy,S.J., Bosak,S.A., McGowan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Mortley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bonifard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalka,U., Smalls,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12479932
2 (bases 1 to 1618)
Strauberg,R.
Direct Submission
Submitted (01-JUN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palokvics
cDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-sngc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 57 Row: n Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9966780.
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SEFNSVSLTVY"
ORIGIN
Alignment Scores:
Pred. NO.: 5.03e-238 Length: 1618
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrPheTyrSerSerTyrVal1G1AlaSer1Le 40
Db 388 ACATGCTGTCATGCTGCTCCAGCTGAAAAACAAGTTCTTATGTCGATCCAGCAT 447
Qy 41 ValThrAlaValG1PheSerTyrG1LeuTyrMetG1uCyAlaThrAlaSerThrG1Y 60
Db 448 GTGACAGAGTGTGCTCTCCAAAGGCTCTGATGATGATGTCACACACAGACAGGC 507
Qy 61 IleThrG1uCyAspPheTyrSerThrLeuLeuG1LeuProAlaAsp11LeG1Ala1Ala 80
Db 508 ATCACCCAGTGTGACATCTATAGACCCCTTCTGGGCTGCGCTGACATCCAGCTGCC 567
Qy 81 G1AlaMetMetVal1ThrSerSerAla11LeSerSerLeuAlaCy11LeSerVal1 100
Db 568 CAGGCAATGATGTGACATCCAGTCAATCTCTCCCTGGCTGATTAATCTCTGTGTG 627
Qy 101 G1MetArgCyThrVal1PheCyG1uG1uSerArg1AlaYAspArgVal1AlaVal1Ala 120

Db 628 GGATGATGACACAGCTTCTGCGCAGAAATCCGAGCAAGAGAGTGGCGGTAGCA 687
Qy 121 G1G1G1YAlaPhePheIleuGlyIleuLeuGlyPheIleProValAlaTTPaLeu 140
Db 688 GGTGAGACTTTTTCATCTTGAGGCTCTCGGATTCATCTCTGTGCTCGGATCTT 747
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Qy 161 G1G1G1uAlaLeuTyLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
Db 808 GAGAGGCTCTTTCATCTTGCGCATTTCTTCCCTGTTTCTCGATAGCGGATCATC 867
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Qy 201 GlnProLeuAlaThrArgSerSerProAArgProGlyGlnProPolysValLysSerGlu 220
Db 928 CAACCTCTTGCCACAGAGACTCTCCAGGCTGCTCACTCCCAAGTCAAGAGTGAAG 987
Qy 221 PheAAsSerTySerLeuThrgIYTyVal 230
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AF177340
LOCUS AF177340 1918 bp mRNA linear PRI 03-OCT-2000
DEFINITION Homo sapiens clone SP82 claudin 2 mRNA, complete cds.
ACCESSION AF177340
VERSION AF177340.1 GI:10503979
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1918)
AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y., Yu,J. and Han,L.H.
TITLE Novel human cDNA clone with function of inhibiting cancer cell growth
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1918)
AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y., Yu,J. and Han,L.H.
TITLE Direct Submission
JOURNAL Submitted (06-AUG-1999) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie Tu Road, Shanghai 200032, P.R. China
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Alignment Scores:

Pred. No.: 5,97e-238

Length: 1918

1918

Score: 230.00 Matches: 230
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9 Gaps: 0
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Db 520 ATGGCTCTTCTGCTCCCAACTTGCGGTGCTATCTTACGCTTCTGCGGCTTTGGGC 579
Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValAlaSerIle 40
Db 580 ACACTGTTCCAGTCTGCTCCCAAGCTGGAAGAACAGTTCATGCGGTGCGAGCAT 639
Qy 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrgly 60
Db 640 GTGACAGCACTTGGCTTCTCCAGGCGCTTGATGGAATGTGCAACAGCAGCAGGC 699
Qy 61 IleThrglnCysAAsPilleTySerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 700 ATCACCCAGTGAACATCTATACACCTTCTGCGCTGCGCTGACATCCAGGCTGCC 759
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 760 CAGGCCATGATGAGATCAGATCAGATCTCTCCCTGCGCTGATATCTGTGCTG 819
Qy 101 G1YMeArGcYsThrValPheCySgInGlnLysArGAlaLysAAsPaRgValAlaValAla 120
Db 820 GGATGATGATGACACAGCTTCTGCGAGGATCCGAGCCAAAGACAGAGTGGCGGTAGCA 879
Qy 121 G1G1YAlaPhePheIleuGlyIleuLeuGlyPheIleProValAlaTTPaLeu 140
Db 880 GGTGAGCTTTTTCATCTTGGAGGCTCTGAGATTCATCTCTGCTGCTGGAATCTT 939
Qy 141 HiG1YIleLeuAArgAAsPheTySerProLeuValProAAsPheMetLysPheGluIle 160
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Qy 161 G1G1uAlaLeuTyLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
Db 1000 GAGAGGCTCTTACTTGGGCAATTTCTTCCCTGTTCTCCGATAGCTGGAATCATC 1059
Qy 181 LeuCyPheSerCySerSerGlnAArgAAsArgSerAntyTyTyraPaAlaTyGlnAla 200
Db 1060 CTCGCTTTTCTGCTCATCTCCAGAAATGCTCCAACTACTGATGCTTACCAAGCC 1119
Qy 201 GlnProLeuAlaThrArgSerSerProAArgProGlyGlnProPolysValLysSerGlu 220
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Qy 221 PheAAsSerTySerLeuThrgIYTyVal 230
Db 1180 TTCATTCTTACAGCTCGACAGGCTATGTG 1209
Search completed: December 20, 2004, 19:27:51
Job time : 4303 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 16:50:21 ; Search time 497 Seconds
(without alignments)
2429.310 Million cell updates/sec

Title: US-09-787-677a-3
Sequence: 1 MASLGQLQVYITGLGLG.....PGQPPKVSFPNSYSLTGYV 230

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 413486 seqs, 2624710521 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8266295

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdt
-LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
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10: geneseqn2003cs:.*
11: geneseqn2003ds:.*
12: geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	100.0	1400	2	AAK97865 Human sec
2	230	100.0	1400	10	ADJ45986 Novel hum
3	230	100.0	1400	12	ADP18800 Human sec
4	230	100.0	1475	3	AAA37060 Human PRO
5	230	100.0	1475	4	AAFS4296 DNA encod
6	230	100.0	1475	4	AAAS21489 Human CDN

7	230	100.0	1475	4	AAAS15360 cDNA enco
8	230	100.0	1475	4	AAFP2097 Human PRO
9	230	100.0	1475	6	ABST74417 Human CDN
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11	230	100.0	1475	6	ABKL11089 cDNA enco
12	230	100.0	1475	6	ABLP95656 Human ang
13	230	100.0	1475	8	ACAS1203 Novel hum
14	230	100.0	1475	8	ACD81580 Human CDN
15	230	100.0	1475	8	ACA60402 Novel hum
16	230	100.0	1475	8	ACA03848 cDNA enco
17	230	100.0	1475	8	ACA58849 cDNA enco
18	230	100.0	1475	8	ABX89386 DNA enco
19	230	100.0	1475	8	ACA4025 cDNA enco
20	230	100.0	1475	8	ACA91289 cDNA enco
21	230	100.0	1475	8	ACD45188 Human sec
22	230	100.0	1475	8	ACD42040 Human sec
23	230	100.0	1475	8	ACA93736 Human CDN
24	230	100.0	1475	8	ACA67310 cDNA enco
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26	230	100.0	1475	8	ACA04269 Human CDN
27	230	100.0	1475	8	ACD02337 Novel hum
28	230	100.0	1475	8	ACA89328 Novel hum
29	230	100.0	1475	8	ACA68965 Novel hum
30	230	100.0	1475	8	ACA98487 Human PRO
31	230	100.0	1475	8	ACA53412 cDNA enco
32	230	100.0	1475	9	ADA46010 Novel hum
33	230	100.0	1475	9	ADA76441 Human PRO
34	230	100.0	1475	9	ADBI1736 Human CDN
35	230	100.0	1475	9	ADA19091 Human PRO
36	230	100.0	1475	9	ADA61714 Homo sapi
37	230	100.0	1475	9	ADBI9499 Novel hum
38	230	100.0	1475	9	ADB28040 cDNA enco
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40	230	100.0	1475	9	ADBI6083 Human PRO
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ALIGNMENTS

RESULT 1
ID AAK97865 standard; cDNA; 1400 BP.
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AC AAK97865;
DT 23-SEP-1999 (first entry)
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DE Human secreted protein encoding cDNA #53.
XX
KW Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;
KW diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
XX
OS Homo sapiens.
XX
PN WO9925825-A2.
XX
PD 27-MAY-1999.
XX
XX 13-NOV-1998; 98WO-IB001862.
XX
XX 13-NOV-1997; 97US-0066677P.
XX 17-DEC-1997; 97US-0069957P.
PR 09-FEB-1998; 98US-0074121P.
PR 13-APR-1998; 98US-0081563P.
PR 10-AUG-1998; 98US-0096116P.
PR 04-SEP-1998; 98US-0099273P.
XX
PA (BEST) GENSET.

PI Bougueleret L, Duclert A, Dumas Milne Edwards J;
 XX WPI: 1999-347472/29.
 DR P-PSDB; AAY36181.
 XX Extended cDNAs encoding secreted proteins.
 XX Claim 1; Page 254-255; 307pp; English.
 CC AAY97813-X97906 represent extended cDNA's which encode novel human
 CC secreted proteins (see AAY36129-Y36222) and which have cytostatic,
 CC thrombotic and osteopathic activity. The extended cDNAs can be used to
 CC express secreted proteins or parts of them or to obtain antibodies
 CC capable of binding to the secreted proteins. They may also be used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC Uses also include design of expression vectors and secretion vectors
 XX
 SQ Sequence 1400 BP; 326 A; 392 C; 346 G; 336 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6.38e-212 Length: 1400
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
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 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 Db 36 ATGGCTCTCTTGGCTTGCCTCACTGTGGGCTACATCTTGGGCTTGGGCTTGGGCT 95
 QY 21 ThrIleuValAlaMetIleuLeuProSerTrpIleThrSerSerTyrValGlyAlaSerIle 40
 Db 96 ACATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 155
 QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
 Db 156 GTGACAGCAGTGGCTTCCAGGGCTCTGAGTGAATGTCCACACACACAGCAGC 215
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 Db 216 ATCACCCAGTGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCAGGCTGCC 275
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 276 CAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 335
 QY 101 GlyMetArgCysThrValPheCysGlnIleSerArgAlaIleAspArgValAlaValAla 120
 Db 336 GGCATGAGATCAGACAGTCTTCTGCCAGAAATCCAGACCAAGACAGAGTGGCGTAGCA 395
 QY 121 GlyIleValPhePheIleLeuGlyLeuGlyPheIleProValAlaIleTrpAsnLeu 140
 Db 396 GGTGAGAGCTTTTTCATCTTGGAGGCTCTCGGAGTTCATCTTGGAGTTCATCTTGGAGTTC 455
 QY 141 HisIleIleLeuAlaGAspPheTyrSerProIleuValProAspSerMetIlePheGluIle 160
 Db 456 CATGGAGTCTTCAAGGAGCTTCTTACCTGACACTGGGCTGACAGATGAAATTTGAGATT 515
 QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 Db 516 GGAAGAGCTCTTACTTGGCATTTTCTTCCCTGTTCTCCCTGATAGCTGGATATCTC 575
 QY 181 LeuCyPheSerCysSerSerGlnArgAlaArgAlaArgSerAlaTyrIleAspAlaTyrGlnAla 200
 Db 576 CTCTGCTTTTCTGCTCATCCAGAGAAATGCTTCACTACATGATGATGATGATGATGATGATG 635
 QY 201 GlnProIleAlaThrArgSerSerProArgProGlyGlnProProIleValIleSerGlu 220
 Db 636 CAACTCTTGGCACAGAGGCTTCCAGAGGCTGTGTCACTCCCAAGATCAAGAGTAG 695

QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 696 TTCAATTCTTACAGCCTGACAGGATATCTG 725
 RESULT 2
 ID ADJ45986 standard; cDNA; 1400 BP.
 XX ADJ45986;
 AC ADJ45986;
 XX 06-MAY-2004 (first entry)
 DT
 XX Novel human secreted protein-related cDNA sequence SeqID139.
 DE
 XX secreted protein; upstream regulator; gene therapy; protein purification;
 KW protein synthesis; chromosomal mapping; individual identification;
 KW forensic; hereditary disease; drug reaction; immunosassay;
 KW epitope mapping; vaccine; immune system regulation;
 KW haematopoietic system; tissue growth; reproductive hormone;
 KW cell migration; blood clotting; receptor/ligand interaction;
 KW adhesion molecule; assisted drug delivery;
 KW human glial maturation factor gamma-2; neurite outgrowth;
 KW neurite resprouting; human; gene; ss.
 KW Homo sapiens.
 XX US2003144490-A1.
 PN 31-JUL-2003.
 XX 10-DEC-2002; 2002US-00319763.
 XX 13-NOV-1997; 97US-0066677P.
 PR 17-DEC-1997; 97US-0069957P.
 PR 09-FEB-1998; 98US-0074121P.
 PR 13-APR-1998; 98US-0081563P.
 PR 10-AUG-1998; 98US-0096116P.
 PR 04-SEP-1998; 98US-0099273P.
 PR 13-NOV-1998; 98US-0019197P.
 PR 15-SEP-2000; 2000US-00663600.
 XX (EDMA/) EDWARDS J D M.
 PA (DUC/L) DUCLERT A.
 PA (BOU/G) BOUGUERET L.
 XX Edwards JDM, Duclert A, Bougueleret L;
 PI WPI: 2003-851788/79.
 DR P-PSDB; ADJ46033.
 XX New nucleic acid encoding secreted human polypeptides, useful e.g. in
 PT gene therapy or diagnosis, also encoded proteins, potential therapeutic
 PT agents.
 PS Claim 3; SEQ ID NO 139; 269pp; English.
 XX This invention relates to novel purified isolated polynucleotides which
 CC comprise a sequence that encodes at least 10 amino acids (aa) from any of
 CC 48 secreted polypeptide sequences, given in the specification, or
 CC fragments of polypeptides encoded by human cDNA contained in the
 CC corresponding deposited clone. The DNA sequences of the invention encode
 CC secreted proteins (or their fragments) and can be used to
 CC identify/isolate upstream regulators, potentially useful in gene therapy
 CC or protein purification, by controlling protein synthesis, as probes for
 CC chromosomal mapping, identification of individuals, and for diagnosis or
 CC forensics, for example identifying genes associated with hereditary
 CC diseases or drug reactions, for recombinant expression of the encoded
 CC proteins or, where the DNA sequence encodes a signal peptide, for
 CC directing secretion of heterologous polypeptides. Polypeptides encoded by
 CC the DNA sequences of the invention can be used to raise antibodies,
 CC useful for detecting the polypeptide, as (ant)agonists, or for preparing
 CC anti-idiotypic antibodies, as tags in for example immunosassays, epitope
 CC mapping or vaccines, also as molecular weight markers, to screen for

CC agents with biological activity and as therapeutic agents with.
CC potentially, a very wide range of activities, for example regulation of
CC the immune or hematopoietic systems, tissue growth, reproductive
CC hormones, cell migration, blood clotting or receptor/ligand interaction,
CC also as adhesion molecules for assisted drug delivery. A typical isolated
CC sequence is human glial maturation factor gamma-2, which stimulates
CC neurite outgrowth and resprouting. The present sequence is a cDNA
CC sequence which encodes a human secreted protein of the invention.

XX SQ Sequence 1400 BP; 326 A; 392 C; 346 G; 336 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.38e-212	Length:	1400
Score:	230.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-787-677A-3 (1-230) x ADP18800 (1-1400)

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QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
Db 36 ATGGCCCTCTTGCGCTCCCAACTGTGGGCTACATCCAGGCTTCTGGGGCTTTGGGC 95
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValGlyAlaSerIle 40
Db 96 ACACTGGTTCCTCAAGCTGCTCCAGCTGAGAAACAAGTTCCTTATGTCGGGCGCAGCAT 155
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaIleThrHisSerThGly 60
Db 156 GTGACAGCAAGTGGCTTCTCCAGAGGCTCTGAGTGAATGTGCACACACAGACAGGC 215
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 216 ATCAACCCAGTGTGACATCTATAGCACCTTCTGGGCGCTCCGCTGACATCAGGCTGCC 275
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValAl 100
Db 276 CAGGCGCATGATGGAGACATCAGACATCTCCCTCGGCTCCATTAATCTCTGTGGTG 335
QY 101 G1WetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
Db 336 GGCATGAGATGACAGATCTTCTGCCAGGAATCCGAGCCAAAGACAGATGGCGGTAGCA 395
QY 121 G1yG1yValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaATPAsnLeu 140
Db 396 GGTGAGATCTTTTTCATCTTGGAGGCTCTCTGGGATTCATCTCTGTTGGCTGGAATCTT 455
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 456 CATGGGATCTTACCGGAGCTTCTACTCACCACTGGTGGCTGACACAGAAATTTGAGATT 515
QY 161 G1yGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 516 GGAAGAGCTCTTAACTTGGGATTAATTTCTCCCTGTTCTCCGATAGACGGAATATC 575
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 576 CTCGCTTTTCTGCTCATCCCAAGAAATGCTCCCAACTACTACGATGCTTCAAGGCC 635
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
Db 636 CAACCTCTTGCACAGAGAGCTCTCCAAAGGCTGTCAACCTCCCAAGTCAAGAGAGTGA 695
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 696 TTCATTCTTACAGCTGACAGGATATGTG 725
RESULT 3
ADP18800
ID ADP18800 standard; cDNA; 1400 BP.
```

```
AC ADP18800;
XX 26-AUG-2004 (first entry)
DT Human secreted polynucleotide #56.
XX Human secreted polynucleotide #56.
DE Human, secreted protein; gene; ss; genetic disease.
XX Homo sapiens.
XX US2004110939-A1.
XX 10-JUN-2004.
XX 15-OCT-2001; 2001US-00978360.
XX 17-DEC-1998; 98WO-IB002122.
XX 09-FEB-1999; 99WO-IB000282.
XX 21-JUN-2000; 2000WO-IB000951.
XX 15-SEP-2000; 2000US-00663600.
XX (BEST ) GENSET SA.
XX Dumas M,Ine Edwards J, Bougueleret L, Joberet S, Clusel C;
PI Duclert A;
XX WPI; 2004-440404/41.
XX P-PSDB; ADP19205.
XX New isolated polynucleotide encoding secreted polypeptide, useful for
PT gene therapy, or in diagnostic procedures to identify individuals having
PT genetic diseases resulting from abnormal expression of the genes.
XX Claim 1; SEQ ID NO 56; 113pp; English.
XX The invention relates to human cDNA sequences that encode human secreted
XX proteins. The invention also relates to an antibody that specifically
XX binds to a polypeptide of the invention and a method of binding the
XX polypeptide to an antibody. The polynucleotides are useful for expressing
XX the entire secreted proteins which they encode and for distinguishing
XX human tissues and cells from non-human tissues and cells, and for
XX distinguishing between human tissues and cells that do or do not express
XX the polynucleotides comprising the cDNAs. The polynucleotides and
XX polypeptides are useful in forensic procedures or diagnostic procedures
XX to identify individuals with genetic diseases resulting from abnormal
XX expression of the genes corresponding to the cDNAs. The sequences are
XX also useful in gene therapy to control or treat genetic diseases. This
XX sequence represents a human secreted polynucleotide of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html.
SQ Sequence 1400 BP; 326 A; 392 C; 346 G; 336 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 6.38e-212 Length: 1400
XX Score: 230.00 Matches: 230
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 12 Gaps: 0
XX
XX US-09-787-677A-3 (1-230) x ADP18800 (1-1400)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
Db 36 ATGGCCCTCTTGCGCTCCCAACTGTGGGCTACATCCAGGCTTCTGGGGCTTTGGGC 95
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValGlyAlaSerIle 40
Db 96 ACACTGGTTCCTCAAGCTGCTCCAGCTGAGAAACAAGTTCCTTATGTCGGGCGCAGCAT 155
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaIleThrHisSerThGly 60
```

Db 156 GTGACAGAGTTGGCTTCCAGAGGCTCTGGATGGATGGACACAGACAGAGGC 215
Qy 61 I1ethrGlnCyAspI1eTySerTh1leuLeuGlyLeuPro1aAspI1eGlnAla1a 80
Db 216 ATCCAGCGGTGACATCTATAGCACCTTCTGGGCTCCCGCTGACATCCAGGCTGCC 275
Qy 81 Gln1aMetMetVal1ThrSerSerAla1eSerSer1eua1aCy1e1eSerVal1a 100
Db 276 CAGGCCATGATGGACATCCAGTGCATCTCTCCCTGGCTGATTAATCTGTGTG 335
Qy 101 GlyMetArgCySerTh1aPheCyAsGln1uSerArgAla1yAspArgVala1aVala1a 120
Db 336 GGCATGAGATCAGACAGCTTCTGCGCAGGATCCGACCAAGACAGAGTGGCGGTACCA 395
Qy 121 GlyGlyValPhePhe1leLeuGlyGlyLeuLeuGlyPhe1leProVala1a1eTrpAsnLeu 140
Db 396 GGTGAGCTTTTTCATCTCTGAGGCTCCTGGGATTCATCTCTGCTGGATCTT 455
Qy 141 HisGly1leuArgAspPheTySerPro1eua1aProAspSerMet1yPheGlu1le 160
Db 456 CATGGATCTTACGGAGCTTCTACTCACCAGCTGTGCTGACAGCATAAATTGAGATT 515
Qy 161 GlyGlnAlaLeuTy1eLeuGly1le1eSerSer1euaPheSer1eua1eGly1le1e 180
Db 516 GGAGAGGCTCTTACTTCTGGCATTATTCTTCCCTGTTCTCCGTGATGCGAATATC 575
Qy 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAnt1yTy1aAspAla1TyGlnAla 200
Db 576 CTGCTCTTTCTGCTCATCCAGAGAAATGCTTCCACTCTACGATGCTTACCAAGCC 635
Qy 201 GlnPro1eua1a1ThrArgSerSerProArgProGlyGlnProPro1yVal1ySerGlu 220
Db 636 CAACCTCTTGCCACAGAGCTCTCCAGGCTGTCACTCTCCAAAGTCAAGAGTGG 695
Qy 221 PheAsnSer1ySer1euaThnGlyTyVal 230
Db 696 TTCAATTCCTACAGCTGACAGGATGTG 725

RESULT 4
ID AAA37060 standard; cDNA; 1475 BP.
XX AAA37060;
AC
XX 08-AUG-2000 (first entry)
DT
XX Human PRO1356 (UNQ705) cDNA sequence SEQ ID NO:133.
DE
XX Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KM transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX Homo sapiens.
OS
XX WC200012708-A2.
PN
XX 09-MAR-2000.
PD
XX 01-SEP-1999; 99WO-US020111.
PF
XX 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.

PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102070P.
PR 29-SEP-1998; 98US-0102076P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 30-SEP-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 14-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105002P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105265P.
PR 26-OCT-1998; 98US-0105633P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.

PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
XX
XX (GERTH) GENENTECH INC.
XX
PI Baker KP, Boltschtein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
PI Pan J, Peoni NF, Roy MA, Smith V, Stewart RA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2001-071395/08.
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
XX PT useful as hybridization probes, in chromosome and gene mapping and gene
XX therapy.
XX
XX Claim 2; Fig 77; 787p; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
XX These proteins and the DNA encoding them may be used as hybridization
XX probes, in chromosome and gene mapping and in the generation of anti-
XX sense RNA and DNA. They may also be used to generate either for
XX transgenic animals or knockout animals which are in turn useful for
XX development and screening of therapeutically useful reagents. The nucleic
XX acids may also be used in gene therapy
XX
SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,72e-212 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-787-677a-3 (1-230) x AAF54296 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGly 20
Db 122 ATGGCTCTCTTGGGCTTCACTGTGGGCTAACAATCCAGGCTTTGGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpIleThrSerSerTyrValGlyAlaSerIle 40
Db 182 ACACGGTGGCCAGTGTCTCCCAAGGCTGGAACCAAGTTCTTATGTGGTCCAGCATT 241
QY 41 ValThrAlaValAlaGlyPheSerIleGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 242 GTGACAGAGATTGGCTTCCAAAGGCTCTGGAGGATGTGCACACACAGCAGCAGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCAACCCAGTGTGACATCTATAGCACCCCTTGGGCTCCCGCTGATCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaValAspArgValAlaValAla 120
Db 422 GGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 481
QY 121 GlyGlyValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTyrAsnLeu 140
Db 482 GGTGAGCTTTTTCATCTTGAAGGCTCTGGGATTCATCTCTGTTGCTGGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlePheGlnIle 160
Db 542 CATGGAGTCTTACGGAGCTTCTACTCACCTGGTGTGCTGACAGCATGAAATTTGAGATT 601
QY 161 GlyAlaIleLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180

Db 602 GGAGAGCTCTTACTGATGAGCATATTTCTCCCTGTTCCTCGATAGCTGGAATCATC 661
QY 181 LeuCybPheSerCysSerSerGlnArgAsnArgSerSerTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCTCGCTCATATCCAGAAATCGCTCAACTAAGTGGCTTCCAGGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValIleSerGlu 220
Db 722 CAACCTTTTGGCAGAGAGCTCTCCAGGCTGTGTCACTCCCAAGTCAGAGAGTGA 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCATTCTTACAGCTGACAGGATGATGTG 811

RESULT 6
AAS21489
ID AAS21489 standard; cDNA; 1475 BP.
XX
XX AAS21489;
AC
XX
XX 24-OCT-2001 (first entry)
DT
XX
XX Human cDNA sequence encoding for PRO1356 polypeptide.
DE
XX
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIa; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200140466-A2.
PN
XX
XX 07-JUN-2001.
PD
XX
XX
XX
XX 01-DEC-2000; 2000WO-US032678.
PF
XX
XX
XX 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030939.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000US-0187202P.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 10-NOV-2000; 2000MO-US030873.
 XX
 PA (GETH) GENENTECH INC.
 PI Baker KP, Beresini M, DeForge L, Deenoyers L, Filvaroff E, Gao W,
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR MPI; 2001-408281/43.
 DR P-PSDB; AAU12417.
 XX
 PT Isolated , secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT breast, prostate, cervical.
 PT
 XX
 PS Claim 3; Fig 491; 813pp; English.
 XX
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 CC
 XX
 SO Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

 Alignment Scores:
 Pred. No.: 6,72e-212 Length: 1475
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

 US-09-787-677A-3 (1-230) x AAS21489 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 DB 122 ATGGCCCTCTTGGCTCCCAACTGTTGGCTACATCTTAAGCCCTTGGGCTTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
 DB 182 ACACTGGTTGGCATGCTGCTCCAGCTGAAAAACAAGTTCTTATGTCGGTCCAGCAT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrPheGlyCysAlaThrAlaSerThrGly 60
 DB 242 GTGACACAGTGGCTTCTCCAAAGGCTCTGATGAAATGTGCAACACAGACAGAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 DB 302 ATCAACCAAGTGTACATCTAAGCACCTTCTGGGCTGCGGTGACATCCAGAGTCC 361
 QY 81 GlnAlaMetMetValTyrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 362 CAGGCAATGATGGATCATCAAGTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 421

QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaAla 120
 DB 422 GGCAATAGATGACACAGCTTCTTCCAGGAATCCCGACCAAAACAGAGTGGGTAGCA 481
 QY 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTyrPheLeu 140
 DB 482 GGTGAGATCTTTTTCATCTTGAAGGCTCTGGGATTCATCTTGGTGGTGAATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlePheGluIle 160
 DB 542 CATGGATCCTACGGACCTTCACTACACACTGGTGGCTGACAGCATGAATTTGAGATT 601
 QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleIleIle 180
 DB 602 GAGAGAGCTCTTACCTGGCATTAATTTCTTCTCTCTCTGATGAGATTCATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAspArgSerAspTyrTyrAspAlaTyrGlnAla 200
 DB 662 CTCTGCTTTTCTGCTCATCTCCAGAAATCGTCCAACTACTACATGCTTCCAAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIleValIleSerGlu 220
 DB 722 CAACCTTGTCCCAAGAGAGCTTCCAGGCTGTGTCACCTCCAAAGTCAGAGTGAAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 782 TTCAAATTCCTACAGCTGACAGGATGATG 811

 RESULT 7
 AAS15360
 ID AAS15360 standard; cDNA; 1475 BP.
 XX
 AC AAS15360;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE cDNA encoding human PRO1356 polypeptide.
 XX
 KW Human; PRO1356; clone DNA64886-1601; immune-related disorder;
 KW inflammatory disorder; infectious disorder; immunodeficiency disorder;
 KW autoimmune disorder; renal disease; demyelinating disease; skin disease;
 KW neoplasia; transplantation associated disease; gene therapy;
 KW immunosuppressive; anti-inflammatory; antidiabetic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 122..814
 FT /*tag= a
 FT /product= "PRO1356 polypeptide"
 FT /tag= b
 FT mat_peptide 194..811
 FT /*tag= c
 FT
 PN WO200166740-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 01-MAR-2001; 2001MO-US006666.
 XX
 XX 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191015P.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 01-DEC-2000; 2000MO-US032678.
 XX
 PA (GETH) GENENTECH INC.
 PI Eaton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL,
 PI Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI: 2001-625876/72.
 DR P-PSDB; AAU09178.
 XX Nucleic acids encoding PRO polypeptides, useful for detecting and
 PT treating immune related diseases and disorders in mammals including
 PT autoimmune diseases, inflammatory diseases and asthma.
 XX
 PS Claim 2; Fig 1; 122pp; English.
 XX
 CC The present invention relates to the isolation of 9 novel human PRO
 CC polypeptides (AAU09178-AAU09186) and the cDNA sequences encoding them.
 CC The novel PRO polypeptides include PRO1356, PRO1884, PRO3444,
 CC PRO3151, PRO3322, PRO9964, PRO10008 and PRO19598. The cDNA sequences
 CC encoding these PRO polypeptides have been designated as clones DN64886-
 CC 1601, DN64903-1553, DN649318-2520, DN67997, DN69273, DN62223-2567,
 CC DN696973, DN6101921 and DN6145887 respectively. Compositions (e.g.
 CC vaccines) containing PRO polypeptides and methods of using these
 CC compositions are useful in the treatment and diagnosis of immune-related
 CC disorders. Such disorders include immune-mediated inflammatory disorders
 CC (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g.
 CC diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis),
 CC immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g.
 CC rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis),
 CC demyelinating diseases of the peripheral or central nervous system (e.g.
 CC Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact
 CC dermatitis), neoplasias and transplantation associated diseases. The
 CC polynucleotide sequences of the invention may be used in gene therapy.
 CC AAS15360-AAS15368 represent cDNA sequences encoding for the novel human
 CC PRO polypeptides of the invention
 CC
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,72e-212 Length: 1475
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-787-677A-3 (1-230) x AAS15360 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
 Db 122 ATGGCTCTCTTGGCTTCAACTGTGGCTACATCTTCAAGCTTCTGGGCTTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrrpYsrThrSerSerTyrValGlyAlaSerIle 40
 Db 182 ACACGTGGTTCATGCTGCTCCCGACGTGAACAAATTCTTAATGTCGGGCCAGCATT 241
 QY 41 ValThrAlaValAlGlyPheSerIleGlyLeuTrrpMetGluCyValAlaThrHisSerThrGly 60
 Db 242 GTGACAGCAGTGGCTTCTCCAAAGGCTCTGGAGATGTGCCACACAGCAGCAGC 301
 QY 61 IlleThrgInCyAspPrlleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
 Db 302 ATCACCCTGCTGACATCTTAAGCACCTTCTGGGCTGCGCGCTGACATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCyValIleIleSerValVal 100
 Db 362 CAGGCGATGATGGTGAATCCAGTCAATCTCTCCGCGCTGATTAATCTGTGGTG 421
 QY 101 GlyMetAlaGlyThrValPheCyGlnGlnSerAlaValAlaValAspValAlaValAla 120
 Db 422 GGCATGAGATCACAGTCTTCTGCCAGGAATCCCGAGCAAAAGACAGTGGCGGTACA 481
 QY 121 GlyGlyValAlaPhePheIleLeuGlyLeuLeuGlyPheIleProValAlaTrrpAsnLeu 140
 Db 482 GGTGAGCTCTTTTATCTTGGAGGCTTCTGGGATTCATCTTGTGCTGGAGATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlePheGlnIle 160

Db 542 CATGGATCTTACGGGACTTCTACTACACACGTGGCTGCAGCATGAATTTGAGATT 601
 QY 161 GlyGlnAlaLeuTyrIleLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 Db 602 GGAGAGGCTCTTATCTTGGGCAATTAATTTCTTCTGTCTCCGATGATGATATC 661
 QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTrrpAspAlaTyrGlnAla 200
 Db 662 CTCGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTACTACATGCTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValIleSerGlu 220
 Db 722 CAACCTTGTGCACAGAGCTCTCCAAAGCTGTGTCACCTCCCAAGTCAGAGTGA 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 782 TTCATCTTACAGCTGACAGGATATGTG 811
 RESULT 8
 ID AAF92097 standard; cDNA; 1475 BP.
 XX AAF92097;
 AC AAF92097;
 XX 15-MAY-2001 (first entry)
 DT
 XX Human PRO1356 cDNA.
 DE
 XX Human; PRO protein; mapping; ss.
 XX Homo sapiens.
 OS
 XX WO200116318-A2.
 PD 08-MAR-2001.
 XX 24-AUG-2000; 2000WO-US023328.
 PF
 XX 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 07-DEC-1999; 99US-0169495P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 25-APR-2000; 2000US-0199397P.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 05-JUN-2000; 2000US-0209832P.
 PA (GERTH) GENENTECH INC.
 XX Aaron DL, Flivaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 XX WPI: 2001-183260/18.
 DR P-PSDB; AAB87565.
 XX
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 PT biology, including use as hybridization probes, and in chromosome and
 PT gene mapping.
 PS Claim 2; Fig 79; 278pp; English.
 XX
 CC The present sequence is the coding sequence for a human PRO polypeptide
 CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
 CC antagonists or anti-PRO antibodies are useful for preparation of a
 CC medicament useful in the treatment of a condition which is responsive to
 CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO

CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping

SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6,72e-212	Length:	1475
Score:	230.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-787-677A-3 (1-230) x AAF92097 (1-1475)

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QY      1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB      122 ATGGCTCTCTTGGCTCCACCTTGAGGCTACCTAGGCTTCTGGGGCTTTGGGC 181
QY      21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
DB      182 ACAGTGTTCGACAGCTGCTCCAGCTGGAACCAAGTTCTTATGCGGTCCAGCATT 241
QY      41 ValThrAlaValGlyPheSerLeuGlyLeuTyrMetGluCysAlaThrIleSerThrGly 60
DB      242 GTGACAGACAGTGGCTTCTCCAGGGCTCTGAGTGAATGTCCACACACAGCAGGC 301
QY      61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProIleAspIleGlnAla 80
DB      302 ATCAACCCAGTGTGACATCTATAGCACCTTCTGGGCTGCGGTGACATCCAGCTGCC 361
QY      81 GlnAlaMetMetValIrrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB      362 CAGGCCATGATGGGATCATCAGTCAATCTCCCTGGGCTGCAATTATCTGTGTG 421
QY      101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaValAla 120
DB      422 GGCATGAGATGACACAGCTTCTTCCAGGAATCCCGACCAAGACAGAGTGGCGTAGCA 481
QY      121 GlyGlyValPhePheIleLeuGlyIleLeuGlyIlePheIleProValAlaIrrAspLeu 140
DB      482 GGTGGATCTTCTTTCATCTTGAGGCTCTCTGGGATTCATCTGTGCTTGGATCTT 541
QY      141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetCysPheGluIle 160
DB      542 CATGGGATCTTACGGGATCTTACTACACACTGTGCTGACAGCATGAATTTGAGATT 601
QY      161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
DB      602 GGAGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTTCCCTCGATAGCTGGAATCATC 661
QY      181 LeuCyPheSerCysSerSerGlnArgAspArgSerIrrTyrAspAlaTyrGlnAla 200
DB      662 CTCTGCTTCTTCCGCTCATCCAGAGAAATGCTCCACACTACATACGATGCTTACAGGCC 721
QY      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValIleSerGlu 220
DB      722 CAACCTTTCGACCAAGAGCTCTCCAGGCTGTGTAACCTCCCAAGTCAAGAGTGAG 781
QY      221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB      782 TTCATTTCTTACAGCTGACAGGATATGTG 811
```

RESULT 9

ABST74417
ID ABST74417 standard; cDNA; 1475 BP.

XX ABST74417;

DT 10-DEC-2002 (first entry)

DE Human cDNA encoding secreted/transmembrane protein PRO1356.

XX Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;

KW antiarthritic; osteopathic; sports-related joint problem;

KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.

OS Homo sapiens.

PN US2002119130-A1.

XX 29-AUG-2002.

PF 06-DEC-2001; 2001US-00006867.

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XX 29-OCT-1997; 97US-0063435P.
XX 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100663P.
PR 16-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 17-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99MO-US005028.
PR 14-MAY-1999; 99MO-US010733.
PR 02-JUN-1999; 99MO-US012252.
PR 01-SEP-1999; 99MO-US020111.
PR 15-SEP-1999; 99MO-US021090.
PR 15-SEP-1999; 99MO-US021194.
PR 22-DEC-1999; 99MO-US030720.
PR 18-FEB-2000; 2000MO-US004341.
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PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023378.
 PR 10-NOV-2000; 2000MO-US030873.
 PR 01-DEC-2000; 2000MO-US032378.
 PR 20-DEC-2000; 2000MO-US034956.
 PR 28-FEB-2001; 2001MO-US006666.
 PR 01-MAR-2001; 2001MO-US006666.
 PR 30-MAY-2001; 2001MO-US017443.
 PR 01-JUN-2001; 2001MO-US017890.
 PR 20-JUN-2001; 2001MO-US019692.
 PR 29-JUN-2001; 2001MO-US021066.
 PR 09-JUL-2001; 2001MO-US021735.
 XX (GERTH) GENENTECH INC.
 PA Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WT;
 XX WPI; 2002-731348/79.
 DR P-PSDB; ABG95890.
 XX
 PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.
 XX
 PS Claim 2; Fig 79; 399pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis
 CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence encodes a novel secreted or transmembrane protein of the

CC invention
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,72e-212 Length: 1475
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-09-787-677A-3 (1-230) x ABS74417 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 DB 122 ATGGCTCTCTGGCTCTCACTGTGGCTACATCTTAGGCTTCTGGGCTTTTGGCC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrIleThrSerSerTyrValGlyAlaSerIle 40
 DB 182 ACACTGGTTGCCATGCTGCTCCCAAGTGAACAAAGTTCTTATGTCGGTCCAGCATT 241
 QY 41 ValThrAlaValGlyPheSerTyrGlyLeuTyrMetGlyCysAlaThrHisSerThrGly 60
 DB 242 GTGACAGCAGTGGCTCTCCAGGGCTCTGTGATGGAATGTGCACACACAGCAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
 DB 302 ATCCACCAAGTGTGACATCTATAGACCTTCTGGGCTTGGCCGTGACATCCAGGCTGCC 361
 QY 81 GlnAlaMetCysValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 362 CAGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaAlaValAlaValAla 120
 DB 422 GGCACTGAGATGACAGATCTTCTGACAGAAATCCGACCAAGACAGAGTGGCGGTGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrAsnLeu 140
 DB 482 GGTGAGCTTTTCACTTCTGAGGCTCTGGGATTCCTTCTTGGCTGGAACTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 DB 542 CATGGATTCCTAGCGGACTTCTACTACCACTGGTGTGCTGACAGATGAATTTGAGATT 601
 QY 161 GlyGluAlaLeuTyrLeuGlyTyrIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 DB 602 GGAAGAGCTCTTTCCTTCTGGGCTATTTCTTCTTCTTCTGATGATGCTGGAATCATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 DB 662 CTGCTCTTCTCTCTCACTCCAGAGAAATGCTCCCACTACAGATGCTTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
 DB 722 CAACCTCTTGCACAGAGAGCTCCCAAGGCTGTGCTCACTCCCAAGTCAAGAGTGAAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 782 TTCAATTCCTACACCTGACAGGCTGATGCTG 811
 RESULT 10
 ABL8167
 ID ABL8167 standard; cDNA; 1475 BP.
 XX ABL8167;
 AC
 XX 16-MAY-2002 (first entry)
 DT
 XX Human PRO1356 cDNA sequence SEQ ID NO:191.
 DE
 XX Human; angiogenesis; cardiac; cytoskeletal; antiangiogenic; hypotensive;

KW vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiotensin disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping; gene; ss.
 XX Homo sapiens.
 OS WO20020690-A2.
 PN 03-JAN-2002.
 PD 20-JUN-2001; 2001WO-US019692.
 PF 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001US-00066666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Garney AJ, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephen JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2002-090516/12.
 DR P-PSDB; ABB84912.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g., myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX Claim 2; Fig 191; 565pp; English.
 CC ABB88072 to ABB88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.

CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABB88259 to ABB88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Score: 6,72e-212 Length: 1475
 Percent Similarity: 230.00 Matches: 230
 Best Local Similarity: 100.00% Conservative: 0
 Query Match: 100.00% Mismatches: 0
 DB: 6 Gaps: 0
 US-09-787-677A-3 (1-230) x ABB88167 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 Db 122 ATGGCCTCTTGGCCCTCAACTGTGGCTACATCTTAGCCCTTGGGGCTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheTyrSerTyrValGlyAlaSerIle 40
 Db 182 ACACTGGTTCACATGCTGCTCCAGCTGAGAAACAAGTTCCTAATGCGGTGCAGCATT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluGlyAlaThrHisSerThGly 60
 Db 242 GTGACAGCACTGGCTTCTCAAGGGCTCTGAGTGAAGTGCACACACAGCACAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
 Db 302 ATCACCCAGTGTGACATCTATAGACCCCTCTGGGCTGCCGTGACATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 Db 362 CAGGCCATGATGTGATGATCATCAGTGCATGATCTCTCCCTGCGCATTAATCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaVal 120
 Db 422 GGCATGATGATCCAGATCTTCTGCGAGATATCCAGACCAAGACAGTGGCGTATGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyLeuGlyPheIleProValAlaTyrPasnLeu 140
 Db 482 GGTGGAGTCTTTTTCATCTTGGAGGCTCTCGGATTAATCTCTGTGCTGGAACTT 541
 QY 141 HisGlyIleLeuAlaArgAspPheTyrSerProLeuValProAspSerMetIysPheGlu 160
 Db 542 CATGGGATCTTACGGGACTTCTTACTCACCACTGGTGTCTACAGCATGAATTTGAGATT 601
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 Db 602 GGAAGGCTCTTACTTGGCATTAATTTCTCCCTGTTCCCTGATAGCTGGAATATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 662 CTCGCTTTTCCGCTCATATCCAGAGAAATCGCTCAACTACATACATGCTCCAAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIysValIysSerGlu 220
 Db 722 CAACCTCTTCCCAAGAGACTCTCCAAAGGCTCGTCACTCCCAAGTCAAGAGTGAAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 782 TTCAATTCCTACAGCTGACAGGATATGTG 811
 RESULT 11
 ABBK1089
 ID ABBK1089 standard; cDNA; 1475 BP.
 XX

XX	OS	Homo sapiens.
XX	FN	W0200208284-A2.
XX	PD	31-JAN-2002.
XX	PF	09-JUL-2001; 2001WO-US021735.
XX	PR	20-JUL-2000; 2000US-0219556P.
XX	PR	25-JUL-2000; 2000US-0220624P.
XX	PR	25-JUL-2000; 2000US-0220664P.
XX	PR	28-JUL-2000; 2000WO-US020710.
XX	PR	02-AUG-2000; 2000US-0222695P.
XX	PR	17-AUG-2000; 2000US-00643657.
XX	PR	23-AUG-2000; 2000WO-US023328.
XX	PR	24-AUG-2000; 2000WO-US023328.
XX	PR	07-SEP-2000; 2000US-0230978P.
XX	PR	18-SEP-2000; 2000US-00664610.
XX	PR	18-SEP-2000; 2000US-00665350.
XX	PR	24-OCT-2000; 2000US-0242922P.
XX	PR	08-NOV-2000; 2000US-00709238.
XX	PR	08-NOV-2000; 2000WO-US030952.
XX	PR	10-NOV-2000; 2000WO-US030873.
XX	PR	01-DEC-2000; 2000WO-US032678.
XX	PR	20-DEC-2000; 2000US-00747259.
XX	PR	20-DEC-2000; 2000WO-US034956.
XX	PR	22-JAN-2001; 2001US-00767609.
XX	PR	28-FEB-2001; 2001US-00766498.
XX	PR	28-FEB-2001; 2001WO-US006520.
XX	PR	01-MAR-2001; 2001WO-US006566.
XX	PR	09-MAR-2001; 2001US-00802706.
XX	PR	14-MAR-2001; 2001US-00808689.
XX	PR	22-MAR-2001; 2001US-00816744.
XX	PR	05-APR-2001; 2001US-00828366.
XX	PR	10-MAY-2001; 2001US-00854208.
XX	PR	10-MAY-2001; 2001US-00854280.
XX	PR	25-MAY-2001; 2001US-00866028.
XX	PR	25-MAY-2001; 2001US-00866034.
XX	PR	25-MAY-2001; 2001WO-US017092.
XX	PR	30-MAY-2001; 2001US-00870574.
XX	PR	30-MAY-2001; 2001WO-US017443.
XX	PR	01-JUN-2001; 2001WO-US017800.
XX	PR	20-JUN-2001; 2001WO-US019692.
XX	PA	(GERTH) GENTECH INC.
XX	PA	(BAKE/) BAKER K P.
XX	PA	(FERR/) FERRARA N.
XX	PA	(GERB/) GERBER H.
XX	PA	(GERR/) GERRITSEN M E.
XX	PA	(GODD/) GODDARD A.
XX	PA	(GODO/) GODOWSKI P J.
XX	PA	(GURN/) GURNEY A L.
XX	PA	(HILL/) HILLAN K J.
XX	PA	(MARS/) MARSTERS S A.
XX	PA	(PANJ/) PAN J.
XX	PA	(PAON/) PAONI N F.
XX	PA	(STEP/) STEPHAN J F.
XX	PA	(WATA/) WATANABE C K.
XX	PA	(WILL/) WILLIAMS P M.
XX	PA	(WOOD/) WOOD W I.
XX	PI	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
XX	PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
XX	PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX	XX	WPI; 2002-171999/22.
XX	DR	P-PSDB; ABB95518.
XX	PT	One hundred and eighty seven nucleic acids encoding PRO polypeptides
XX	PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX	PT	infarction), endothelial or angiohenic disorders in a mammal.

PS Claim 1; Fig 191; 567bp; English.

XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention
XX

80 Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6,72e-212	Length:	1475
Score:	230.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-787-677A-3 (1-230) x ABU95656 (1-1475)

QY	1	MetAlaSerLeuEngLyLeuGlnLeuValGlyTYRlleEngLyLeuLeuEngLyLeuEngLy	20
Db	122	ATGGGCTCTCTGGGCTCCCACTTGTGGCTCACTCACTCACTTGTGGGCTTGTGGGCTTTGGGCT	181
QY	21	ThreLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTYrValGlyAlaSerIle	40
Db	182	ACACTGTGTCATCTGCTCTCCCACTGAGAAACAAAGTTCTTATCTCGGTCCAGCATT	241
QY	41	ValThrAlaValAlGlyPheSerLySgLyLeuTrpMetGluCYeAlaThrHisSerThrgLy	60
Db	242	GTCACAGCAGATTGGCTTCTCCAAAGGGCTCTGATGGATGGCCACACACAGCACAGGC	301
QY	61	IleThrGlnCYAspIleTYrSerThrLeuLeuEngLyLeuProAlaAspIleGlnAlaAla	80
Db	302	ATCACCCAGTGGATCATCTATAGCACCCCTTCTGGGGCTGCCGCTGACATCCAGCGCTGCC	361
QY	81	GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCYarIleIleSerValVal	100
Db	362	CAGGCGCATGATGTATACATCCAGTGAACTCTCTCCCTGCAATATCTCTGTGTGTG	421
QY	101	GlyMetArgCYsThrValPheCYeGlnGlnSerArgAlaAlaAspArgValAlaValAla	120
Db	422	GGCATGATGATGCACAGCTCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCA	481
QY	121	GlyGlyValPhePheIleLeuGlyGlyLeuLeuEngLyPheIleProValAlaTrpAsnLeu	140
Db	482	GGTGAAGTCTTTTTCATCTCTTGAAGGCTCTGGGATTCATTCTGTGCTCGGAATCTT	541
QY	141	HisGlyIleLeuArgAspPheTYrSerProLeuValProAspSerMetLysPheGluIle	160
Db	542	CATGGATCTCAACGGGACTCTTACATCACACACGAGGCTCGAAGACATGGAATTTGAGATT	601
QY	161	GlyGlnAlaLeuTYrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle	180
Db	602	GGAGAGGCTCTTAACTTGGGCAATTATTTCTTCCCTGTTCTCCCTGATAGCTGAATCATC	661
QY	181	LeuCYsPheSerCYsSerSerGlnArgAsnArgSerAsnTYrTYrAspAlaTYrGlnAla	200
Db	662	CTGTGCTTTTCTGCTCATCCAGAGAAATGCTCCAACTACTAGATGCTCTCAAGCC	721
QY	201	GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu	220
Db	722	CAACCTCTTGCCACAGAGAGCTCTCCAAAGGCTGTGTCACTCCCAAAGTCAAGAGTGAG	781
QY	221	PheAsnSerTYrSerLeuThrgLyTYrVal	230
Db	782	TTCAATTCTTACAGCTTACAGGAGGATATGTG	811

RESULT 13
ACA91203

ID ACA91203 standard; cDNA; 1475 BP.
XX
AC ACA91203;
XX
DT 11-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1356 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antibody therapy;
KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003018173-A1.
XX
PD 23-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063515.
XX
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Baton DL, Filvaroff E, Gerltzen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI,
XX
DR WPI; 2003-401702/38.
DR P-PSDB; AB090915.
XX
PT New antibody useful for identifying PRO polypeptides, for affinity
PT purification of PRO polypeptides, and for preparing a medicament for
PT diagnosing or treating conditions responsive to the antibody or PRO
PT polypeptide.
XX
PS Disclosure; Fig 79; 345bp; English.
XX
CC The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostics, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 6.72e-212 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 230
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-787-677a-3 (1-230) x ACA91203 (1-1475)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
DB 122 ATGGCTCTTCTGGGCTCAACTGTGTGGCTACATCTCAGGCTTCTGGGCTTTTGGGC 181
QY 21 ThrIleuValAlaMetLeuLeuProSerTyrIleTyrSerSerTyrValGlyAlaSerIle 40
DB 182 ACACGTGTTGCCATCTCTCCCGCAGTGAAGAAACAAGTTCTTATGTGCGTGCAGCAT 241
QY 41 ValThrAlaValAlaGlyPheSerIleGlyLeuTyrMetGluGlyAlaThrHisSerThrGly 60
DB 242 GTGACAGCAGTGTGCTTCCAAAGGCTCTGAGATGATGCGCACACAGCAGCAGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80

DB 302 ATCACCCAGTGTGACATCTATAGACCCCTCTGGGCTGCCCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaValAla 120
DB 422 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
QY 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTyrPheLeu 140
DB 482 GGTGAGCTTTTTCATCTTGGAGGCTCTGAGGATTCATCTTCTGCTGAGATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetCysPheGluIle 160
DB 542 CATGGATCTTACCGGCTTCTACTCACCTGCTGATGATGATGATGATGATGATGATG 601
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
DB 602 GGAGAGCTCTTTCATCTTGGGCTTATTTCTTCTCTGATGATGATGATGATGATGATG 661
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAntTyrTyrAspAlaTyrGlnAla 200
DB 662 CTCTGCTTTTCTCTGCTCATCCAGAGAAATCGCTCCAACTAGTACGATGCTACCAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlySValIleSerGlu 220
DB 722 CAACTCTTTCACCAAGAGCTCTCCAAAGCTGTGTCACCTCCCAAGATCAAGAGTGA 781
QY 221 PheAsnSerTyrSerLeuTyrGlyTyrVal 230
DB 782 TTCAATCTTACAGCTGACAGGATATGTG 811
RESULT 14
ACD81580
ID ACD81580 standard; cDNA; 1475 BP.
XX
AC ACD81580;
XX
DT 18-SEP-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1356.
DE Human; secreted/transmembrane protein; PRO; tumour; cancer;
KW Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;
KW cytosolic.
XX
OS Homo sapiens.
XX
PN US2003009013-A1.
XX
PD 09-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063519.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99WO-US012384.
PR 30-DEC-1999; 99WO-US013174.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-0064610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-DEC-2001; 2001US-00006867.
 PA (GENTH) GENENTECH INC.
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Matanabe CK, Wood WI;
 PI WPI; 2003-447384/42.
 DR P-PSDB; ABO33974.
 XX
 XX New isolated antibody specifically binding a PRO polypeptide, useful for
 PT the preparation of a medicament for treating disorders with the aberrant
 PT expression or activity of the PRO polypeptide, such as tumor conditions
 PT and cancer.
 XX
 XX Disclosure; Fig 79; 223p; English.
 PS
 XX
 XX The invention relates to an antibody that binds to a secreted or
 CC transmembrane protein designated PRO1446 appearing as ABO33941. The
 CC protein is one of 84 PRO polypeptides which (along with their encoding
 CC nucleic acids) are disclosed in the specification. The methods and
 CC compositions of the present invention are useful for the preparation of a
 CC medicament for the treatment of disorders associated with the aberrant
 CC expression or activity of the PRO polypeptide, such as tumor conditions
 CC and cancer. They can also be used to generate transgenic or knockout
 CC animals useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
 CC molecular weight markers for protein electrophoresis, chromosome
 CC identification and tissue typing. The antibodies may be used in various
 CC diagnostic, competitive binding and/or immunoprecipitation assays. The
 CC present sequence encodes a PRO polypeptide
 CC
 XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 6 72e-212 Length: 1475
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0
 US-09-787-677A-3 (1-230) x ACDB1580 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
 DB 122 ATGGCTCTCTTGCGCTTCACTGTGGCTACATCTTCCAGGCTTTGGGGCTTTGGGC 181
 QY 21 ThrIleuValAlaMetLeuLeuProSerTrpIleThrSerSerTrpValGlyAlaSerIle 40
 DB 182 ACACCTGGTTGGCAGCTGCTCCACGCGAAGAAACAGATTCTTATGTCGGGCGCAGCAT 241
 QY 41 ValThrAlaValGlyIlePheSerLeuGlyLeuTrpMetGluCysAlaThrIleSerThrGly 60
 |||||||

DB 242 GTGACAGAGTTGGCTTCTCCAGGGCTCTGATGATGATGTCACACAGCAGCAGC 301
 QY 61 IleThrGlnCysAspIleIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
 DB 302 ATCACCCAGTGTGACATCTATAGACACCTTCTGGGCTGCGCGGTGACATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 362 CAGGCAATGATGGATGATCAGTCAATCTCTCCCTGGGCTGCAATTAATCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaIleAspArgValAlaValAla 120
 DB 422 GCGATGATGATGACAGCTTCTGCGAGGATCCGAGCCAAAGACAGAGTGGCGTGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyIleLeuLeuGlyPheIleProValAlaIlePheLeu 140
 DB 482 GGTGAGCTTTTTCATCTTGAGGCTCTCGGATTCATTCCTGTGCTGGAAATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlePheGluIle 160
 DB 542 CATGGATCTTACGGGACTTCTACTCACCTGCTGCTGACATGAATGAATTTGAGATT 601
 QY 161 GlyAlaAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 DB 602 GGAGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTTCCCTGATGCTGAAATCATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaIleGlnAla 200
 DB 662 CTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTAGTACGATGCTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValIleSerGlu 220
 DB 722 CAACCTCTTGCACCAAGAGCTCTCCAAAGGCTGTGTCACCTCCCAAGTCAAGAGTGA 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 782 TTCAATTCCTACAGCTCGACAGGATATGTG 811
 RESULT 15
 ID ACA60402 standard; cDNA; 1475 BP.
 XX
 AC ACA60402;
 XX
 DT 11-JUN-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO1356 cDNA.
 XX
 KW Human, secreted and transmembrane polypeptide; gene;
 KW 88, chromosome mapping; gene mapping; transgenic animal; knockout animal;
 KW therapeutic agent screening; chromosome identification; tissue typing;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 FN US2003018183-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 01-MAY-2002; 2002US-00063512.
 XX
 PR 06-DEC-2001; 2001US-00006867.
 XX
 XX (GENTH) GENENTECH INC.
 PA
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Matanabe CK, Wood WI;
 PI WPI; 2003-330984/31.
 DR P-PSDB; ABU71991.
 DR
 XX New secreted and transmembrane PRO polypeptides and nucleic acid
 PT molecules encoding the polypeptides, useful in gene therapy or preparing

PT a medicament for treating a condition that is responsive to the PRO
PT polypeptide or antibody.
XX Disclosure; Fig 79; 409pp; English.

XX The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide

XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.72e-212 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-787-677a-3 (1-230) x ACN60402 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGly 20
Db 122 ATGGCTCTCTTGGCTCCCACTGTGGGTACATCTTAGGCTTCTGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpIleThrSerSerTyrValGlyAlaSerIle 40
Db 182 ACAGTGTGGTCCATGCTGCTCCCAAGGAAACAGTCTTATGTGGTCCAGCAAT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 242 GTGACAGCATTTGGCTTCCAGGAGCTCTGGATGATGTGCCACACACAGCAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCCAGTGTGACATCTATAGCACCTTCTGGGCTGCCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGAGTACATCCAGTCAATCTCTCCCTGGCTGATTAATCTCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
Db 422 GGCATGATGATGACAGCTTCTTCCAGAGAAATCCGAGCCAAAGACAGATGGCGGTAGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleTrpAsnLeu 140
Db 482 GGTGGAGTCTTTTTCATCTTGGAGGCTCTCTGGGATTCATTCCTGTGCTGGATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlePheGlnIle 160
Db 542 CATGGATCTTACGGGATCTTACTACACACTGGTGTGCTGACAGCATGATAATTTGAGATT 601
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAAGAGCTCTTACTTGGCATTTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATC 661
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCTGTCTATCCAGAGAAATGCTCTCACTACTAGATGCTTACCAAGCC 721

QY 201 GlnProLeuAlaPheArgSerSerProArgProGlyGlnProProValIleSerGlu 220
Db 722 CAACCTTTGGCACACAGAGCTCTCCAGGCTGTGTTCACTCTCCAAAGTCAAGAGTGA 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCAATTCCTACAGCTGACAGGGGTATGTG 811

Search completed: December 20, 2004, 18:16:05
Job time : 501 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 18:07:46 ; Search time 95 Seconds
(without alignments)
1720.857 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 230
Sequence: 1 MASLGLVGLVGLGLGLG.....PGQPKVSEFNSYSLTGV 230

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1643622

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame-p2n.model -DEV=xlh
-Q=/cgnt_1/USPTO.spool/US09787677/rn1at.20122004.132818.19789/app.query.fasta_1.391
-DB=Issued Patents NA -OPMT=fastap -SUFFIX=oli.rn1 -MINMATCH=0.1 -LOOPTCL=0
-LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human0.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptco -NORM=ext -HEA=SITE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09787677 @CGN1.1.69 @rn1at.20122004.132818.19789 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

- 1: /cgnt_6/prodata/1/ina/5A_COMB.seq:*
- 2: /cgnt_6/prodata/1/ina/5B_COMB.seq:*
- 3: /cgnt_6/prodata/1/ina/6A_COMB.seq:*
- 4: /cgnt_6/prodata/1/ina/6B_COMB.seq:*
- 5: /cgnt_6/prodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgnt_6/prodata/1/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	100.0	1400	4	US-09-663-600A-139 Sequence 139, App
2	230	100.0	1475	4	US-10-140-002-491 Sequence 491, App
3	127	55.2	1524	4	US-09-663-600A-45 Sequence 45, Appl
4	5	3.9	627	4	US-09-252-991A-6070 Sequence 6070, Ap
5	4	3.9	630	4	US-09-252-991A-6398 Sequence 6398, Ap
6	3	3.9	873	4	US-09-252-991A-6226 Sequence 6226, Ap
7	8	3.5	410	3	US-09-114-146-1 Sequence 1, Appl1
8	8	3.5	410	5	PCT-US96-08623-1 Sequence 1, Appl1
9	8	3.5	417	4	US-09-252-991A-257 Sequence 257, App
10	8	3.5	709	2	US-08-844-120-2 Sequence 2, Appl1
11	8	3.5	709	2	US-09-022-940-2 Sequence 2, Appl1
12	8	3.5	709	3	US-09-216-386-2 Sequence 2, Appl1

13	8	3.5	709	3	US-09-213-394-2 Sequence 2, Appl1
14	8	3.5	714	4	US-09-252-991A-1683 Sequence 1683, Ap
15	8	3.5	753	4	US-09-270-767-1386 Sequence 1386, Ap
16	8	3.5	753	4	US-09-270-767-1386 Sequence 1668, A
17	8	3.5	846	4	US-09-270-767-12047 Sequence 12047, A
18	8	3.5	930	4	US-09-252-991A-1404 Sequence 1404, Ap
19	8	3.5	1002	4	US-09-252-991A-11872 Sequence 11872, A
20	8	3.5	1008	4	US-09-248-796A-3558 Sequence 3558, Ap
21	8	3.5	1284	3	US-09-134-001C-212 Sequence 212, App
22	8	3.5	1386	4	US-10-182-263-9 Sequence 9, Appl1
23	8	3.5	1386	4	US-10-182-263-10 Sequence 10, Appl1
24	8	3.5	1386	4	US-10-182-263-11 Sequence 11, Appl1
25	8	3.5	1386	4	US-10-182-263-12 Sequence 12, Appl1
26	8	3.5	1389	4	US-09-252-991A-4243 Sequence 4243, Ap
27	8	3.5	1437	4	US-09-252-991A-1434 Sequence 1434, Ap
28	8	3.5	1464	4	US-09-252-991A-11508 Sequence 11508, A
29	8	3.5	1473	4	US-09-252-991A-15508 Sequence 1584, Ap
30	8	3.5	1611	4	US-09-534-743-1 Sequence 1, Appl1
31	8	3.5	1611	4	US-09-534-743-1 Sequence 3, Appl1
32	8	3.5	1629	4	US-09-252-991A-11733 Sequence 11733, A
33	8	3.5	1941	4	US-09-252-991A-248 Sequence 248, App
34	8	3.5	1995	4	US-09-252-991A-14545 Sequence 14545, A
35	8	3.5	2022	4	US-09-252-991A-1152 Sequence 1152, Ap
36	8	3.5	2470	3	US-09-091-725-18 Sequence 18, Appl1
37	8	3.5	2546	3	US-09-091-725-12 Sequence 12, Appl1
38	8	3.5	2598	4	US-09-252-991A-423 Sequence 423, Ap
39	8	3.5	2859	4	US-09-853-180B-1 Sequence 1, Appl1
40	8	3.5	2874	4	US-09-252-991A-4533 Sequence 4533, Ap
41	8	3.5	3084	4	US-09-252-991A-1315 Sequence 1315, Ap
42	8	3.5	3090	4	US-09-016-434-1397 Sequence 1397, Ap
43	8	3.5	3108	4	US-09-614-221A-194 Sequence 194, App
44	8	3.5	3396	4	US-09-252-991A-14676 Sequence 14676, A
45	8	3.5	3444	4	US-09-252-991A-15078 Sequence 15078, A

ALIGNMENTS

RESULT 1
US-09-663-600A-139
; Sequence 139, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Ducleret, Aymeric
; APPLICANT: Bouguetrec, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31 US3 CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent .pm
; SEQ ID NO 139
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: 36..107
; OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 5.6999980926514
 OTHER INFORMATION: seq ILGLGLGLTLVA/ML
 NAME/KEY: polya_signal
 LOCATION: 1302..1307
 NAME/KEY: polya_site
 LOCATION: 1389..1400
 US-09-663-600A-139

Alignment Scores:

Pred. No.:	6.97e-214	Length:	1400
Score:	230.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	4	Gaps:	0

US-09-787-677A-3 (1-230) x US-09-663-600A-139 (1-1400)

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Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly 20
Db 36 ATGGCCCTCTTGGCCCTTCAACTTGTGGCTACATCTTAGGCCCTTGGGGCTTTGGGC 95
Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
Db 96 ACACGTGTGCTGCTGCTGCCACGTGGAACAAAGTTCTTATGTGGTGCCAGCAT 155
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThgIy 60
Db 156 GTACAGACAGATGGCTTCTCCAGAGGCTCTGAGTGAATGTGCACACACAGCAGGC 215
Qy 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db 216 ATCACCCAGGTGACATCTATAGCACCTTCTGGGCTGCCGTGACATCCAGGCTGCC 275
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 276 CAGGCGCATGATGGACATCAGTGCATCTCCCTGGCTGCTCATATCTGTGTGTG 335
Qy 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
Db 336 GGCATGAGATGACAGATCTTCTGACAGAAATCCGAGCCAAAGACAGATGGCGGTAGCA 395
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaATrPAsnLeu 140
Db 396 GGTGGAGCTCTTTTCACTTGTGAGGCTCTCGTGGATTCATCTGTGTGCTGGAATCTT 455
Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 456 CATGGAGTCTTACGGGACTTCTACTCACCACTGGTGTGCTGACACATGAATTTGAGATT 515
Qy 161 GlyGlnAlaLeuTyrIleGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 516 GGAAGAGCTCTTATCTGGGCAATATTTCTTCCCTGATCTCCGATAGCTGGAAATATC 575
Qy 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 576 CTCTGCTTTTCTCTCTCATCTCCAGAAATGCTTCCAACTACTACATGCTTACCAAGCC 635
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
Db 636 CAACCTCTTCCACAAAGAGCTCTCCAAAGGCTGTGCACTCCCAAGTCAAGAGAGAG 695
Qy 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 696 TTCATTCTCAACGCTGACAGGGGTATGTG 725

```

RESULT 2
 US-10-140-002-491
 Sequence 491 Application US/10140002

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen

```

APPLICANT: DeForge, Laura
APPLICANT: Denoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Mei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 491
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-002-491

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Alignment Scores:

Pred. No.:	7.33e-214	Length:	1475
Score:	230.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	4	Gaps:	0

US-09-787-677A-3 (1-230) x US-10-140-002-491 (1-1475)

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Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly 20
Db 122 ATGGCCCTCTTGGCCCTTCAACTTGTGGCTACATCTTAGGCCCTTGGGGCTTTGGGC 181
Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
Db 182 ACACGTGTGCTGCTGCTGCCACGTGGAACAAAGTTCTTATGTGGTGCCAGCAT 241
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThgIy 60
Db 242 GTACAGACAGATGGCTTCTCCAGAGGCTCTGAGTGAATGTGCACACACAGCAGGC 301
Qy 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db 302 ATCACCCAGGTGACATCTATAGCACCTTCTGGGCTGCCGTGACATCCAGGCTGCC 361
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 362 CAGGCGCATGATGGACATCTATAGCACCTTCTCGTGGCTGCAATATCTGTGTGTG 421
Qy 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
Db 422 GGCATGAGATGACAGATCTTCTCCAGAAATCCGAGCCAAAGACAGAGTGGGTAGCA 481
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaATrPAsnLeu 140
Db 482 GGTGGAGCTCTTTTCACTTGTGAGGCTCTCGTGGATTCATCTGTGTGCTGGAATCTT 541
Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 542 CATGGAGTCTTACGGGACTTCTACTCACCACTGGTGTGCTGACAGCATGAATTTGAGATT 601
Qy 161 GlyGlnAlaLeuTyrIleGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAAGAGCTCTTATCTGGGCAATATTTCTTCCCTGATCTCCGATAGCTGGAAATATC 661

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QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
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QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
DB 722 CAACCTTTCGCCACAGAGAGCTCTCCAGAGCGCTGGGTCAACCTCCCAAGTCAAGAGTGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCATTTCCACAGCGCTGACAGGGTATGTG 811
RESULT 3
US-09-663-600A-45
Sequence 45, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 45
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig peptide
LOCATION: 160..231
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.6999980926514
NAME/KEY: polyA_signal
LOCATION: 1510..1515
NAME/KEY: polyA_site
LOCATION: 1506..1519
NAME/KEY: misc_feature
LOCATION: 1048..1504
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA552647
NAME/KEY: misc_feature
LOCATION: 597..846
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA345449
NAME/KEY: misc_feature
LOCATION: 39..53
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA345449
NAME/KEY: misc_feature
LOCATION: 113..149
OTHER INFORMATION: homology

OTHER INFORMATION: id: AA345449
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 98..400
OTHER INFORMATION: homology
OTHER INFORMATION: id: T86266
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 1210..1489
OTHER INFORMATION: homology
OTHER INFORMATION: id: T86158
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 954..983
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA116709
OTHER INFORMATION: est
US-09-663-600A-45
Alignment Scores:
Pred. No.: 7.03e-114 Length: 1524
Score: 127.00 Matches: 228
Percent Similarity: 98.28% Conservative: 0
Best Local Similarity: 98.28% Mismatches: 2
Query Match: 55.22% Indels: 4
DB: 4 Gaps: 0
US-09-787-677A-3 (1-230) x US-09-663-600A-45 (1-1524)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTyrLeuGlyLeuGlyLeuGly 20
DB 160 ATGGCCCTCTTGAGCTTCCCACTTGAGGCTACATCTTACGCTTCTGGGCTTTGGGC 219
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrTyrThrSerSerTyrValGlyAlaSerIle 40
DB 220 ACACGTGTCCTGCTGCTGCTCCCACTGGAACAAAGTTCTTATGTCGTGCAGCAT 279
QY 41 ValThrAlaValGlyPheSerIysGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
DB 280 GTGACAGCAGTTGGCTTCTCCAGAGCGCTCTGATGGAATGTCCACACACAGCAGGC 339
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGln-AlaAl 80
DB 340 ATCACCCAGTGACATCTATACACCCCTTGGGCTGCGCTGACATCCA-KGCTGC 398
QY 80 aglnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVa 100
DB 399 CCAAGCCATGATGATGATCAATCCAGTCAATCTCTCCCTGCTGATATCTGTGCT 458
QY 100 IglyMetArg-CyThrValPheCysGlnGlnSerArgAlaValAspArgValAlaVal 120
DB 459 GGGCATGAR-ATGCACAGTCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGTAG 517
QY 120 IaglyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTrpAsnL 140
DB 518 CAGGTGAGCTTTTTCATCTTGGAGGCTCTTGAGATTCATCTCTGTGCTGGATC 577
QY 140 euHisGlyIleLeuAAspPheTyrSerProLeuValProAspSerMetLysPheGlnI 160
DB 578 TTCATGGATCCCAACGGAATCTTACTCAACATGATGCTGACAGATGAATTTGAGA 637
QY 160 IeglyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
DB 638 TTGAGAGGCTCTTTCATCTTGGGCAATTAATTCCTCCCTGATGCTGGAATCA 697
QY 180 IeLeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGln 200
DB 698 TCCTCTGCTTTCTCTGCTCATCCAGAGAAATGCTCAACTACATGATGCTTACCAAG 757
QY 200 IaglnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerG 220
DB 758 CCACACTCTTGGCACAGAGAGCTCTCCAGAGGCTGTCAACTCCCAAGTCAAGAGTG 817

Qy 220 IupheanserfYrSerLeuThrGlyTyrVal 230
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Db 818 AGTTCATTCTCTACAGCTCAGCGGATGTG 849

RESULT 4
US-09-252-991A-6070
; Sequence 6070, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6070

; LENGTH: 627

; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-6070

Alignment Scores:

Pred. No.: 10.1 Length: 627
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.91% Indels: 0
DB: 4 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-252-991A-6070 (1-627)

Qy 204 AlathrargserProArgProGly 212
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Db 58 GCGACAGATCATCGCCCGGCTGGC 84

RESULT 5

US-09-252-991A-6398/c
; Sequence 6398, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6398

; LENGTH: 630

; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-6398

Alignment Scores:

Pred. No.: 10.1 Length: 630
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.91% Indels: 0
DB: 4 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-252-991A-6398 (1-630)

Qy 204 AlathrargserProArgProGly 212

Db 550 GCGACAGATCATCGCCCGGCTGGC 524

RESULT 6
US-09-252-991A-6226
; Sequence 6226, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6226

; LENGTH: 873

; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-6226

Alignment Scores:

Pred. No.: 13.8 Length: 873
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.91% Indels: 0
DB: 4 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-252-991A-6226 (1-873)

Qy 204 AlathrargserProArgProGly 212
|||||

Db 320 GCGACAGATCATCGCCCGGCTGGC 346

RESULT 7

US-09-114-146-1
; Sequence 1, Application US/09114146
; Patent No. 6083747

; GENERAL INFORMATION:

; APPLICANT: MONG, Peter M.C.

; APPLICANT: CHUNG, Siu-Wah

; TITLE OF INVENTION: GLYCOPROTEIN GP105 ON BLS HEMATOPOIETIC
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500

CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/114,146

FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/471,188
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 46074/102/FEIN

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-114-146-1

Alignment Scores:
Pred. No.: 62.5 Length: 410
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 3 Gaps: 0

US-09-787-677a-3 (1-230) x US-09-114-146-1 (1-410)

Qy 13 leuGlyLeuLeuGlyLeuLeuGly 20
Db 240 CTGGCCTGCTGGGCGCTGGGCG 263

RESULT 8
PCT-US96-08623-1
Sequence 1, Application PC/RUS9608623
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: GLYCOPROTEIN GPI05 ON BLS HEMATOPOIETIC
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08623
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/471,188
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 46074/103/REIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US96-08623-1

Alignment Scores:
Pred. No.: 62.5 Length: 410
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 3 Gaps: 0

Query Match: 3.48% Indels: 0
DB: 5 Gaps: 0

US-09-787-677a-3 (1-230) x PCT-US96-08623-1 (1-410)

Qy 13 leuGlyLeuLeuGlyLeuLeuGly 20
Db 240 CTGGCCTGCTGGGCGCTGGGCG 263

RESULT 9
US-09-252-991A-257
Sequence 257, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIORITY APPLICATION NUMBER: US 60/074,788
PRIORITY FILING DATE: 1998-02-18
PRIORITY APPLICATION NUMBER: US 60/094,190
PRIORITY FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 257
LENGTH: 417
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-257

Alignment Scores:
Pred. No.: 63.5 Length: 417
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 4 Gaps: 0

US-09-787-677a-3 (1-230) x US-09-252-991A-257 (1-417)

Qy 70 leuLeuGlyLeuProAlaAspIle 77
Db 217 CTGCTGGGCTGCCCGCGACATC 240

RESULT 10
US-08-844-120-2
Sequence 2, Application US/08844120
Patent No. 5858756
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Puri
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDN0T19
CLONE: 2676650
US-08-844-120-2

Alignment Scores:
Pred. No.: 106 Length: 709
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 2 Gaps: 0

US-09-787-677A-3 (1-230) x US-08-844-120-2 (1-709)

QY 12 11leleuglyleuenglyleu 19
DB 169 ATACTGGGCGCTGTAGGCGCTGTTA 192

RESULT 11
US-09-022-940-2
Sequence 2, Application US/09022940
Patent No. 5965423
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,940
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-022-940-2

Alignment Scores:

Pred. No.: 106 Length: 709
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 2 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-022-940-2 (1-709)

QY 12 11leleuglyleuenglyleu 19
DB 169 ATACTGGGCGCTGTAGGCGCTGTTA 192

RESULT 12
US-09-216-386-2
Sequence 2, Application US/09216386
Patent No. 6093561
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,386
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,940
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-216-386-2

Alignment Scores:
Pred. No.: 106 Length: 709
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 3 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-216-386-2 (1-709)

QY 12 11leleuglyleuenglyleu 19
DB 169 ATACTGGGCGCTGTAGGCGCTGTTA 192

RESULT 13
US-09-213-394-2
Sequence 2, Application US/09213394

Patent No. 6319701
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purni
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,394
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNNOT19
CLONE: 2676650
US-09-213-394-2
Alignment Scores:
Pred. No.: 106 Length: 709
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 3 Gaps: 0
US-09-787-677a-3 (1-230) x US-09-213-394-2 (1-709)
Qy 12 l1lelenglyleuenglyleu19
Db 169 ATRCTGGGCTGTAGGCTGTTA 192
RESULT 14
US-09-252-991A-1683
Sequence 1683, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1683
LENGTH: 714
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1683
Alignment Scores:
Pred. No.: 107 Length: 714
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 4 Gaps: 0
US-09-787-677a-3 (1-230) x US-09-252-991A-1683 (1-714)
Qy 204 AlathrArgSerProArgPro 211
Db 345 GCACGAGATCTTCGCCAAGGCC 368
RESULT 15
US-09-270-767-1386
Sequence 1386, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1386
LENGTH: 753
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-1386
Alignment Scores:
Pred. No.: 112 Length: 753
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 4 Gaps: 0
US-09-787-677a-3 (1-230) x US-09-270-767-1386 (1-753)
Qy 206 ArgSerProArgProGlyGln 213
Db 690 CGGTCACTCTCTCGACGAGGCA 713
Search completed: December 20, 2004, 21:25:57
Job time : 97 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 19:27:57 ; Search time 547 Seconds
(without alignments)
2321.376 Million cell updates/sec

Title: US-09-787-677A-3
Perfect score: 230
Sequence: 1 MASLGLVGYILGLLGLG.....PGQPKVKSSEFNSYSTLGYV 230

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Ygapop 60.0 , Ygapext 60.0
Egapop 6.0 , Egapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4093002 seqs, 2760418825 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8176338

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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-DB=Published Applications.NA -QFMT=fastapp -SUFFIX=ol1.rnpb -MIMATCH=0.1
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-TRANS=human0.cci -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09787677 @CGN_1_1.480 @runat.20122004.132820.19878
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-FAPOP=6 -FAPEXT=7 -YGAPOP=60 -YGAEXT=60 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA: *
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11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq: *
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14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq: *
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16: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq: *
17: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	230	100.0	1400	11	US-09-978-360A-56	Sequence 56, App1
2	230	100.0	1400	10	US-10-319-763A-139	Sequence 139, App
3	230	100.0	1475	10	US-09-888-257A-1	Sequence 1, App1
4	230	100.0	1475	10	US-09-946-374-133	Sequence 133, App
5	230	100.0	1475	13	US-10-006-867-79	Sequence 79, App1
6	230	100.0	1475	13	US-10-063-547-79	Sequence 79, App1
7	230	100.0	1475	13	US-10-063-551-79	Sequence 79, App1
8	230	100.0	1475	14	US-10-028-072-491	Sequence 491, App
9	230	100.0	1475	14	US-10-063-616-79	Sequence 79, App1
10	230	100.0	1475	14	US-10-140-808-491	Sequence 491, App
11	230	100.0	1475	14	US-10-063-566-79	Sequence 79, App1
12	230	100.0	1475	14	US-10-063-513-79	Sequence 79, App1
13	230	100.0	1475	14	US-10-063-515-79	Sequence 79, App1
14	230	100.0	1475	14	US-10-063-512-79	Sequence 79, App1
15	230	100.0	1475	14	US-10-121-049-491	Sequence 491, App
16	230	100.0	1475	14	US-10-123-904-491	Sequence 491, App
17	230	100.0	1475	14	US-10-140-470-491	Sequence 491, App
18	230	100.0	1475	14	US-10-063-502-79	Sequence 79, App1
19	230	100.0	1475	14	US-10-175-746-491	Sequence 491, App
20	230	100.0	1475	14	US-10-176-918-491	Sequence 491, App
21	230	100.0	1475	14	US-10-176-921-491	Sequence 491, App
22	230	100.0	1475	14	US-10-063-549-79	Sequence 79, App1
23	230	100.0	1475	14	US-10-137-865-491	Sequence 491, App
24	230	100.0	1475	14	US-10-140-474-491	Sequence 491, App
25	230	100.0	1475	14	US-10-142-431-491	Sequence 491, App
26	230	100.0	1475	14	US-10-143-114-491	Sequence 491, App
27	230	100.0	1475	14	US-10-140-002-491	Sequence 491, App
28	230	100.0	1475	14	US-10-063-554-79	Sequence 79, App1
29	230	100.0	1475	14	US-10-006-856A-133	Sequence 133, App
30	230	100.0	1475	14	US-10-142-419-491	Sequence 491, App
31	230	100.0	1475	14	US-10-063-553-79	Sequence 79, App1
32	230	100.0	1475	14	US-10-063-518-79	Sequence 79, App1
33	230	100.0	1475	14	US-10-123-262-491	Sequence 491, App
34	230	100.0	1475	14	US-10-142-423-491	Sequence 491, App
35	230	100.0	1475	14	US-10-063-596-79	Sequence 79, App1
36	230	100.0	1475	14	US-10-227-693-79	Sequence 79, App1
37	230	100.0	1475	14	US-10-006-818A-133	Sequence 133, App
38	230	100.0	1475	14	US-10-121-050-491	Sequence 491, App
39	230	100.0	1475	14	US-10-141-755-491	Sequence 491, App
40	230	100.0	1475	14	US-10-143-032-491	Sequence 491, App
41	230	100.0	1475	14	US-10-063-563-79	Sequence 79, App1
42	230	100.0	1475	14	US-10-006-485A-133	Sequence 133, App
43	230	100.0	1475	14	US-10-013-907A-133	Sequence 133, App
44	230	100.0	1475	14	US-10-015-499A-133	Sequence 133, App
45	230	100.0	1475	14	US-10-063-555-79	Sequence 79, App1

ALIGNMENTS

RESULT 1
US-09-978-360A-56
; Sequence 56, Application US/09978360A
; Publication No. US20040110939A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouguenere, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56, US4, CIP
; CURRENT APPLICATION NUMBER: US/09/978, 360A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066, 677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069, 957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074, 121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081, 563

PRIOR FILING DATE: 1998-04-13
 PRIOR APPLICATION NUMBER: US 60/096,116
 PRIOR FILING DATE: 1998-08-10
 PRIOR APPLICATION NUMBER: US 60/099,273
 PRIOR FILING DATE: -09-04
 PRIOR APPLICATION NUMBER: US 09/191,997
 PRIOR FILING DATE: 1998-11-13
 PRIOR APPLICATION NUMBER: US 09/215,435
 PRIOR FILING DATE: 1998-12-17
 PRIOR APPLICATION NUMBER: PCT/IB98/02122
 PRIOR FILING DATE: 1998-12-17
 PRIOR APPLICATION NUMBER: US 09/247,155
 PRIOR FILING DATE: 1999-02-09
 Remaining Prior Application data removed - See File wrapper or PALM.
 NUMBER OF SEQ ID NOS: 810
 SOFTWARE: Patent.pm
 SEQ ID NO 56
 LENGTH: 1400
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: sig.peptide
 LOCATION: 36..107
 OTHER INFORMATION: Von Heijne matrix
 OTHER INFORMATION: score 5.6999980926514
 OTHER INFORMATION: seq ILGLGLGLTVA/ML
 FEATURE:
 NAME/KEY: polyA_signal
 LOCATION: 1302..1307
 FEATURE:
 NAME/KEY: polyA_site
 LOCATION: 1389..1400
 US-09-978-360A-56

Alignment Scores:
 Pred. No.: 8,74e-218 Length: 1400
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-978-360A-56 (1-1400)

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 DB 36 ATGGCCCTCTTGGCTTCAACTGTGGCTACATCTTGGGCTTGGGCTTTGGGC 95
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrrPlySerSerTrrValAlaSerTlle 40
 DB 96 ACACGTGTTCCATGCTGCTGCCAGCTGGAACAAAGTTTATTGTGGGCCAGCAT 155
 QY 41 ValThrAlaValGlyPheSerLyGlyLeuTrrMetGlyCysAlaThrHAsSerThGly 60
 DB 156 GTGACAGACAGTGGCTTCTCCAGGGCTCTGATGAAATGTGCCACACACAGCAGGC 215
 QY 61 IleThrGlnCysAspTlleTrrSerThrLeuGlyLeuProAlaAspTlleGlnAla 80
 DB 216 ATCACCAGGTGTGACATCTAAGCACCTTCTGGGCTGCGGCTGACATCCAGGCTGCC 275
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 276 CAGGCCATGATGTGACATCTCAAGTCAATCTCTCTGCGCTCATATTCTGTGTGTG 335
 QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIysAspArgValAlaValAla 120
 DB 336 GGCATGAGATGACACAGTCTTCTGCCAGAAATCCGAGACAAAGACAGAGTGGCGTAGCA 395
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleThrAsnLeu 140
 DB 396 GGTGAGATCTTTTCATCTTGGAGGCTCTCTGGAAATTCATCTGTGCTTGGAAATCTT 455
 QY 141 HisGlyIleLeuArgAspPheTrrSerProLeuValProAspSerMetLysPheGluIle 160

DB 456 CATGGATCTCTAGGGGACTTCTACTCACCACTGGTGGCTGACATGAATTTGAGATT 515
 QY 161 GlyGlnAlaLeuTrrLeuGlyIleIleSerSerLeuPheSerIleuIleAlaGlyIleIle 180
 DB 516 GGAGAGGCTCTTACTTGGGCAATTATTTCTTCCCTGTCCGTAGCTGAATCATC 575
 QY 181 LeuCysPheSerCysSerSerGlnArgAspArgSerAsnTrrTrrAspAlaTrrGlnAla 200
 DB 576 CTCTGCTTTTCTGCTCATCTCCAGAAATCGCTCCAACTACTACATGCTTACCAAGCC 635
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIysValIysSerGlu 220
 DB 636 CAACCTCTTCCCAAGAGACTCTCCAGAGCTGTGTCAACCTCCCAAGTCAAGAGTAG 695
 QY 221 PheAsnSerTrrSerLeuThrGlyTrrVal 230
 DB 696 TTCATTTCTTACAGCTGACAGGGTATGTG 725

RESULT 2

US-10-319-763-139
 Sequence 139, Application US/10319763
 Publication No. US2003014490A1
 GENERAL INFORMATION:
 APPLICANT: Dumas Milne Edwards, Jean-Baptiste
 APPLICANT: Ducleert, Aymeric
 APPLICANT: Bougueleret, Lydie
 TITLE OR INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
 FILE REFERENCE: G-031.US04.DIV
 CURRENT APPLICATION NUMBER: US/10/319,763
 CURRENT FILING DATE: 2002-12-10
 PRIOR APPLICATION NUMBER: 60/066,677
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/069,957
 PRIOR FILING DATE: 1997-12-17
 PRIOR APPLICATION NUMBER: 60/074,121
 PRIOR FILING DATE: 1998-02-09
 PRIOR APPLICATION NUMBER: 60/081,563
 PRIOR FILING DATE: 1998-04-13
 PRIOR APPLICATION NUMBER: 60/096,116
 PRIOR FILING DATE: 1998-08-10
 PRIOR APPLICATION NUMBER: 60/099,273
 PRIOR FILING DATE: 1998-09-04
 NUMBER OF SEQ ID NOS: 229
 SOFTWARE: Patent.pm
 SEQ ID NO 139
 LENGTH: 1400
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: sig.peptide
 LOCATION: 36..107
 OTHER INFORMATION: Von Heijne matrix
 OTHER INFORMATION: score 5.6999980926514
 OTHER INFORMATION: seq ILGLGLGLTVA/ML
 FEATURE:
 NAME/KEY: polyA_signal
 LOCATION: 1302..1307
 FEATURE:
 NAME/KEY: polyA_site
 LOCATION: 1389..1400
 US-10-319-763-139

Alignment Scores:

Pred. No.: 8,74e-218 Length: 1400
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-09-787-677A-3 (1-230) x US-10-319-763-139 (1-1400)

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QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValGlyAlaSerIle 40
DB 96 ACCTGTTGCCATGCTGCTCCAGCTGGAAAACAAGTTCTTATGTCGGTGGCAGATT 155
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
DB 156 GTGACAGCAGTTGGCTTCTCAAGGGCTCTGGATGGAAATGTCACACACACAGGC 215
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlnGlyLeuProAlaAspIleGlnAla 80
DB 216 ATACACCAAGTATGATCTATAGACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 275
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 276 CAGGCGATGATGGTGAATCAGATGCAATCTCTCCCTGGCTGCAATATCTCTGGTGC 335
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaVal 120
DB 336 GGCATGAGATGACAGAGCTTCTGCGCAAGAAATCCGAGCCAAAGACAGAGTGGCGTAGCA 395
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlnGlyPheIleProValAlaTyrPasnLeu 140
DB 396 GGTGGAGCTCTTTTCACTTCTTGAGGCTCTGGGATTCATTCCTGTTGGCTTGAACCTT 455
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
DB 456 CATTGGATCTTACGGAGCTTCTTACTCACACTGGTGTGCTACAGCATGAAATTTGAGATT 515
QY 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 516 GGAGAGGCTCTTACTTGGGCAATTATTTCTTCCCTGTTCTCCCTGATGAGCTGGATCATC 575
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerSerTyrTyrAspAlaTyrGlnAla 200
DB 576 CTCTGCTTTTCCGCTCATCTCCAGAGAAATCGCTCCAACTACACGATGCTTACCAAGCC 635
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 636 CAACCTCTTCCCAACAGAGACTCTCCAGGCTGGTGAACCTCCCAAGTCACAGAGTAG 695
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 696 TTCAATTCTACAGCTGACAGGATATGTG 725

RESULT 3
US-09-888-257A-1
; Sequence 1, Application US/09888257A
; Publication No. US20030060612A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Polakis, Paul
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5002R1
; CURRENT APPLICATION NUMBER: US/09/888,257A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/063,540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: US 60/089,653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/099,792
; PRIOR FILING DATE: 1998-09-10

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; PRIOR APPLICATION NUMBER: US 60/103,678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 60/235,451
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
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; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 1
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-888-257A-1

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Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-787-677A-3 (1-230) x US-09-888-257A-1 (1-1475)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlnLeuGly 20
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QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValGlyAlaSerIle 40
DB 182 ACCTGTTGCCATGCTGCTCCAGCTGGAAAACAAGTTCTTATGTCGGTGGCAGATT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
DB 242 GTGACAGCAGTTGGCTTCTCCAGGCTCTGGATGGAAATGTCACACACACAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlnGlyLeuProAlaAspIleGlnAla 80
DB 302 ATACACCAAGTATGATCTATAGACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 362 CAGGCGATGATGGTGAATCAGATGCAATCTCTCCCTGGCTGCAATATCTCTGGTGC 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaVal 120
DB 422 GGCATGAGATGACAGAGCTTCTCCAGGAAATCCGAGCCAAAGACAGAGTGGCGTAGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlnGlyPheIleProValAlaTyrPasnLeu 140
DB 482 GGTGAGCTCTTTTCACTTCTTGAGGCTCTGGATTCATTCCTGTTGGCTTGAACCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
DB 542 CATTGGATCTTACGGAGCTTCTTACTCACACTGGTGTGACAGCATGAAATTTGAGATT 601
QY 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180

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Db	602	GGAGAGAGCTTACTTACTTGGGACATTTATTTCTCCCTGTTCCCTGATGATGCGAATCATC	661
Qy	181	LeuCybPhSeSerCyseSerSerGlnrArganaArgSerAntyTYTYRApAlaTYGlnAla	200
Db	662	CTGTGCTTTTCCGTGCTCATCCAGAGAAATCGCTCAACTCTAGAGCTTACCAAGCC	721
Qy	201	GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLYValLYSerGlu	220
Db	722	CAACCTCTTGCCACAGAGAGCTCTCCAAAGCGCTGGTCAACCTCCCAAGTCAAGAGGAG	781
Qy	221	PheAsnSerTYSerLeuThrGlyTYrVal	230
Db	782	TTCAATTCTTACAGAGCTGACAGGATATGCG	811
RESULT 4			
US-09-946-374-133			
Sequence 133, Application US/09946374			
Publication No. US20030073129A1			
GENERAL INFORMATION:			
APPLICANT: Baker, Kevin P.			
APPLICANT: Botstein, David			
APPLICANT: Deonoyere, Luc			
APPLICANT: Eaton, Dan L.			
APPLICANT: Ferrara, Napoleone			
APPLICANT: Fong, Sherman			
APPLICANT: Gao, Wei-Qiang			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Grimaldi, Christopher J.			
APPLICANT: Gurney, Austin L.			
APPLICANT: Hillan, Kenneth J.			
APPLICANT: Pan, James			
APPLICANT: Paoni, Nicholas F.			
APPLICANT: Roy, Margaret Ann			
APPLICANT: Smith, Victoria			
APPLICANT: Stewart, Timothy A.			
APPLICANT: Tumae, Daniel			
APPLICANT: Watanabe, Colin K.			
APPLICANT: Williams, P. Mickey			
APPLICANT: Wood, William I.			
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
TITLE OF INVENTION: Acids Encoding the Same			
FILE REFERENCE: P2830P1C1			
CURRENT APPLICATION NUMBER: US/09/946,374			
CURRENT FILING DATE: 2001-09-04			
PRIOR APPLICATION NUMBER: 60/098716			
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PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores: 9.17e-218 Length: 1475
Pred. No.:

Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
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Db 122 ATGGCTCTCTTGGCTCCCACTTGGGCTAATCTTGGGCTTGGGCTTGGGCT 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
Db 182 ACACGTGTGCGCAAGTGTCTCCACCTGAGAAACAGTTCATATGTCGATGCGAGCAT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTyrMetGlyCysAlaThrHisSerThrGly 60
Db 242 GTACACAGCACTTGGCTTCTCCAGAGGCTCTGATGGATGTCCACACACACAGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCAGTGTACATCTATACACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 362 CAGGCATGATGTGTGATCATCATCATCTCTCTGCTGCTGATATCTCTGTGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAla 120
Db 422 GGCATAGATGACATCTTCTCCAGGAATCCAGAACCAACAGAGTGGCGTACGA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrPheLeu 140
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QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlu 160
Db 542 CATGGATCTCTAGGAGACTTACTCATCCACCATGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
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Db 782 TTCATTTCTACAGCTGTACAGGATATGTG 811
RESULT 5
US-10-006-867-79
; Sequence 79, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1

CURRENT APPLICATION NUMBER: US/10/006,867
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/063435
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/064215
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PRIOR APPLICATION NUMBER: 60/101475
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103678
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103679
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103711
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
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PRIOR APPLICATION NUMBER: 60/105881
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PRIOR APPLICATION NUMBER: 60/106030
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PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106856
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108807
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/112419
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/112853
PRIOR FILING DATE: 1998-12-16
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PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/112854
PRIOR FILING DATE: 1998-12-16
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PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113408
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114223
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 60/115614
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116527
PRIOR FILING DATE: 1999-01-20

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PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/119285
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/119287
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/119525
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/120014
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/129122
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/129674
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/138387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/175481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/191007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/199397
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/380139
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380142

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Alignment Scores:

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Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

```

US-09-787-677a-3 (1-230) x US-10-006-867-79 (1-1475)

```

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
DB 122 ATGGCCCTCTTGGCTCCCAATGTTGGCTACATCTTAGGCTTGGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrrpLySerSerTyrValGlyAlaSerIle 40
DB 182 ACCTGGTGGCCATGCTGCTCCCAAGTGAAGAAAGTTCTTATGCGGTGCACGATT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrrpMetGlyCysAlaThrHisSerThrGly 60
DB 242 GTACACGACATTGGCTTCTCCAGGGCTCTGATGGAATGTCACACACAGCACAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
DB 302 ATCAACCAAGTGTACATCTATAGACACCTTCTGGGCTGCGCGTGAATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCCATGATGATGATCAGTCAATCTCCCTGCGCTGCATTATCTGTGAGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlySerAlaIleValAspArgValAlaValAla 120
DB 422 GGCATGATGATGATGATGATCTTCTGCGAGGAATCCGAGCCAAAGACAGAGTGGCGTGCA 481

```

```

QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrrpAlaLeu 140
DB 482 GTTGAGGCTTTTTCATCTTGAGGCTCTCGGAGTATCTCTGTGCTGGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CATGGATCTTACGGAGACTTCTATCTACCACTGCTGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 602 GGAGAGGCTCTTACTTGGGCTATTATTTCTTCCCTGCTTCCCTGATAGCTGAATCATC 661
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTrrpAlaTyrGlnAla 200
DB 662 CTCTGCTTTCCTGCTCATCTCCAGAGAAATGCTCCAACTACTACATGCTTACCAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 722 CAACCTCTTCCCAAGAGACTTCCAGGCTGTGTCAACCTCCCAAGTCAAGAGTGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCAATTCTTACAGCTGACAGGATATGTG 811

```

RESULT 6

US-10-063-547-79
Sequence 79, Application US/10063547
Publication No. US20020182638A1

GENERAL INFORMATION:

```

APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 79
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien

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US-10-063-547-79

Alignment Scores:

```

Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

```

US-09-787-677a-3 (1-230) x US-10-063-547-79 (1-1475)

```

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
DB 122 ATGGCCCTCTTGGCTCCCAATGTTGGCTACATCTTAGGCTTGGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrrpLySerSerTyrValGlyAlaSerIle 40
DB 182 ACCTGGTGGCCATGCTGCTCCCAAGTGAAGAAAGTTCTTATGCGGTGCACGATT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrrpMetGlyCysAlaThrHisSerThrGly 60
DB 242 GTACACGACATTGGCTTCTCCAGGGCTCTGATGGAATGTCACACACAGCACAGGC 301

```

QY 11lethrglnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
DB 302 ATCAACCCAGGTGATGACATCTATAGCACCTTCTGGAGCTGCCCCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCCATGATGGATGACATCCAGGCAATCTCCCTGGGCTGTCATTTATCTCTGTGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaValAspAlaValAla 120
DB 422 GGCATGATGATGACAGAGCTTCTGCGAGAAATCCGAGACCAAGACAGAGTGGCGGTAGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrAsnLeu 140
DB 482 GGTGGAGATCTTTTCACTTCCTGGAGGCTCTGGGATTCATTCCTGTTGCTGGAAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CATGGATCTTACGGGACTTCTACTCAACACTGGTGGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 602 GGAAGGCTCTTACTTGGGCAATATTTCTCCCTGTTCTCCCTGATAGCTGGAAATCATC 661
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
DB 662 CTCGCTTTTCTCTCTCTCTCCAGAGAAATGCTCCACTCACTACATGATGCTTCAAGGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 722 CAACCTCTTGCCACAGAGAGCTCTCCAGGCTGTGTCACCTCCCAAGTCCAGAGTGTGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCATTTCTTACAGCTGACAGGGGTATGTG 811

RESULT 7
US-10-063-551-79
Sequence 79, Application US/10063551
Publication No. US20020183494A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063, 551
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 79
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-551-79

Alignment Scores:
Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-787-677a-3 (1-230) x US-10-063-551-79 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
DB 122 ATGGCTCTTCTGGCTCCCAACTTGTGGCTTACATCTAGGCTTCTGGGCTTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValGlyAlaSerIle 40
DB 182 ACATGGTTSCCATGCTGCTCCCAAGTGAAGAAACAAAGTTCTTATGCGGTGCAGCATT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysValAlaThrHisSerThrGly 60
DB 242 GTACAGACATTTGGCTTCTCCAGAGGCTCTGTGATGAAATGCCACACACAGCAGGC 301
QY 61 11lethrglnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
DB 302 ATCAACCCAGGTGATGACATCTATAGCACCTTCTGGAGCTGCCCCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCCATGATGGATGACATCCAGGCAATCTCCCTGGGCTGTCATTTATCTCTGTGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaValAspAlaValAla 120
DB 422 GGCATGATGATGACAGAGCTTCTGCGAGAAATCCGAGACCAAGACAGAGTGGCGGTAGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrAsnLeu 140
DB 482 GGTGGAGATCTTTTCACTTCCTGGAGGCTCTGGGATTCATTCCTGTTGCTGGAAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CATGGATCTTACGGGACTTCTACTCAACACTGGTGGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 602 GGAAGGCTCTTACTTGGGCAATATTTCTCCCTGTTCTCCCTGATAGCTGGAAATCATC 661
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
DB 662 CTCGCTTTTCTCTCTCTCCAGAGAAATGCTCCACTCACTACATGATGCTTCAAGGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 722 CAACCTCTTGCCACAGAGAGCTCTCCAGGCTGTGTCACCTCCCAAGTCCAGAGTGTGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCATTTCTTACAGCTGACAGGGGTATGTG 811

RESULT 8
US-10-028-072-491
Sequence 491, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-10-29
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PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
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PRIOR FILING DATE: 1997-11-17
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PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
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PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/081695
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PRIOR FILING DATE: 1998-05-12
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414
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PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088730
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07

Alignment Scores:

Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-787-677a-3 (1-230) x US-10-028-072-491 (1-1475)

Qy 1 MetAlaSerLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 122 ATGGCCCTCTTGGCCCTTCACTTGTGGCTTCACTTGTGGCCCTTTTGGCC 181
Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerYrValGlyAlaSerIle 40
Db 182 ACACTGTTGCATGCTGCTCCAGCTGGAAAACAATTCTTATGCGGTGCCAGCAT 241
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGlyCysAlaThrHisSerThGly 60
Db 242 GTGCACACAGTTGGCTTCTCCAGGGCTCTGATGATGTGCACACAGCACAGGC 301
Qy 61 IleThrGlnCysAspIleYrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCAACCAAGTGTGATCTATAGCACTTGTGGCTTGGCCCTGACATCCAGCTGCC 361
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 362 CAGGCCATGATGAGATCAGATCCAGTCAATCCCTCCGCTGCTCATTTATCTGTGTG 421
Qy 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaValAspArgValAla 120
Db 422 GGCGTGTGATGACACAGTCTTCTCCAGGAATCCGAGCAAAAGACAGTGTGCCGTGCA 481
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
Db 482 GGTGTGAGCTTTTTCATCTTGTGAGGCTCTGTGGATTCATCTCTGTGCTGGAATCT 541
Qy 141 HisGlyIleLeuArgAspPheYrSerProLeuValProAspSerMetLysPheGluIle 160

Db 542 CATGGATCTTACAGCACTTCTACTCACCACTGTGCTGCAGACATGAATTTGAGATT 601
Qy 161 GlyGlnAlaLeuYrIleGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAAGGCTCTTACTTGGCATTTATTTCTTCTGTTCTCCGTATGCTGGATCATC 661
Qy 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnYrYrAspAlaIleGlnAla 200
Db 662 CTCTGCTTTCCGCTCATCTCCAGAAATCGCTCCAACTACTACATGCTCCAAAGCC 721
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db 722 CAACCTTTCACCAAGAGACTCTCCAAAGCCCTGTGTCAACTCCCAAAAGTCAAGAGAG 781
Qy 221 PheAsnSerTrpSerLeuThrGlyTyrVal 230
Db 782 TTCATTTCTTACAGCTGTGACAGGGGTATGTG 811

RESULT 9

US-10-063-616-79
Sequence 79, Application US/10063616
Publication No. US20030013855A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 79
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-616-79

Alignment Scores:

Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-787-677a-3 (1-230) x US-10-063-616-79 (1-1475)

Qy 1 MetAlaSerLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 122 ATGGCCCTCTTGGCCCTTCACTTGTGGCTTCACTTGTGGCCCTTTTGGCC 181
Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerYrValGlyAlaSerIle 40
Db 182 ACACTGTTGCATGCTGCTCCAGCTGGAAAACAATTCTTATGCGGTGCCAGCAT 241
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGlyCysAlaThrHisSerThGly 60
Db 242 GTGCACACAGTTGGCTTCTCCAGGGCTCTGATGATGTGCACACAGCACAGGC 301
Qy 61 IleThrGlnCysAspIleYrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCAACCAAGTGTGATCTATAGCACTTGTGGCTTGGCCCTGACATCCAGCTGCC 361
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100

```

Db      362 CAGCCATGATGATGACATCCAGTCAATCTCCTCGGCTGCATATATCTGTG 421
Qy      101 GYMeArGyArThrValPheCySGInGluSerArgAlaLysAspArgValAlaValAla 120
Db      422 GGCATGAGATGACACAGCTCTTCTGCGAGGATCCCGAGCAAGACAGAGTGGGGTGA 481
Qy      121 GYGLYValAlaPheHeiLeuGlyGlyLeuLeuGlyPheHeiLeuValAlaATPAsnLeu 140
Db      482 GGTGGAGCTCTTTCATCTCTTGAGAGCTCTTGAGATTCATCTCTGTGCTGGAATCTT 541
Qy      141 HIsGlyLeuValArgAspPheTySerProLeuValProAspSerMetLysPheGluIle 160
Db      542 CATGGATCTTACGAGACTTCTACTCCACCTGCTGCTACAGCATGAATTTGAGATT 601
Qy      161 GYGLYAlaLeuTyrlLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db      602 GAGAGAGCTCTTACTTGGGCAATTAATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATC 661
Qy      181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrlTyrlAspAlaTyrlGlnAla 200
Db      662 CTCTGCTTTTCCGCTCATCTCCAGAGAAATCGCTCCAACTACTACATGCTTACCAAGCC 721
Qy      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db      722 CAACCTCTTGCCCAAGAGAGCTCTCCAGAGCTGTGTCACCTCCCAAGTCAGAGTGA 781
Qy      221 PheAsnSerTyrlSerLeuThrglyTyrlVal 230
Db      782 TTCATTTCTACAGCTGACAGGGTATGTG 811

```

RESULT 10

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US-10-140-808-491
; Sequence 491, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140, 808
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 491
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-808-491

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Alignment Scores:

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Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

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US-09-787-677a-3 (1-230) x US-10-140-808-491. (1-1475)

```

Qy      1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrlLeuGlyLeuLeuGlyLeuLeuGly 20
Db      122 ATGGCTCTCTTGGCTCCCAATTTGGGGCTGACATCTTCTGCGGGCTTTTGGGC 181
Qy      21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrlValAlaSerIle 40
Db      182 ACACGTGTGGCCATGCTGTCTCCCACTGGAATAAACAAGTTCTTATGTCGTGCACATT 241
Qy      41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrpMetGlyCyValAlaThrHisSerThrgly 60
Db      242 GTACAGCACTTGGCTTCTTCCAAAGGCTCTGATGATGATGCCACACACACAGAGCC 301
Qy      61 IleThrGlnCyAspIleTyrlSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db      302 ATCACCAGATGATCATCTATACACCTTCTGGGCTGCGCTGCGCTGACATCCAGGCTGCC 361
Qy      81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaGlyIleIleSerValVal 100
Db      362 CAGGCCATGATGATGATGATCCAGTCAATCTCTCCCTGCTGCAATATCTGTGTG 421
Qy      101 GYMeArGyArThrValPheCySGInGluSerArgAlaLysAspArgValAlaValAla 120
Db      422 GGCATGAGATGACACAGCTCTTCTGCGAGATCCCGAGCAAGACAGAGTGGGGTGA 481
Qy      121 GYGLYValAlaPheHeiLeuGlyGlyLeuLeuGlyPheHeiLeuValAlaATPAsnLeu 140
Db      482 GGTGGAGCTCTTTCATCTCTTGAGAGCTCTCGGATTCATCTCTGTGCTGGAATCTT 541
Qy      141 HIsGlyLeuValArgAspPheTySerProLeuValProAspSerMetLysPheGluIle 160
Db      542 CATGGATCTTACGAGACTTCTACTCCACCTGCTGCTACAGCATGAATTTGAGATT 601
Qy      161 GYGLYAlaLeuTyrlLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db      602 GAGAGAGCTCTTACTTGGGCAATTAATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATC 661
Qy      181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrlTyrlAspAlaTyrlGlnAla 200
Db      662 CTCTGCTTTTCCGCTCATCTCCAGAGAAATCGCTCCAACTACTACATGCTTACCAAGCC 721
Qy      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db      722 CAACCTCTTGCCCAAGAGAGCTCTCCAGAGCTGTGTCACCTCCCAAGTCAGAGTGA 781
Qy      221 PheAsnSerTyrlSerLeuThrglyTyrlVal 230
Db      782 TTCATTTCTACAGCTGACAGGGTATGTG 811

```

RESULT 11

```

US-10-063-569-79
; Sequence 79, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33230R1C1
; CURRENT APPLICATION NUMBER: US/10/063, 569
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475

```

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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-569-79

Alignment Scores:
Pred. No.:      9,176-218      Length:      1475
Score:          230.00         Matches:      230
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    100.00%        Indels:      0
DB:             14             Gaps:        0

US-09-787-677a-3 (1-230) x US-10-063-569-79 (1-1475)

QY      1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db      122 ATGGCCCTCTTGCCCTCCCACTGTGGGCTACATCTTAGGCCCTTCTGGGGCTTTTGCGC 181
QY      21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerSerTyrValGlyAlaSerIle 40
Db      182 ACACGTGTTGCCATGCTGCTCCCACTGGAACCAAGTTCTTATGTCGGTCCAGCATTT 241
QY      41 ValThrAlaValGlyPheSerIleGlyLeuTyrPheGlyCysAlaThrHisSerThrGly 60
Db      242 GTGACAGCAGTTGGCTTCTCCAAAGGCTCTGATGGAATGTCCACACAGCAGCAGC 301
QY      61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db      302 ATACCCAGGTGACATCTATAGCACCCCTTCTGGGCTGCGCGTGACATCCAGGCTGCC 361
QY      81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValAl 100
Db      362 CAGGCCATGATGGAGCATCATCAGCATCTCTCTCCCTGCGCTCATATCTCTGTGTG 421
QY      101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
Db      422 GGCATGAGATGACAGCTTCTCCAGGAATCCGAGCAAAAGACAGATGGCGGTAGCA 481
QY      121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleTyrAsnLeu 140
Db      482 GGTGGATCTTTTTCATCTTGGAGGCTCTCTGGGATTCATCTCTGTGCTCGGAATCTT 541
QY      141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetCysPheGluIle 160
Db      542 CATGGATCTCTACGGGACTTCTACTCACACTGTGCTGACACAGCAAGAAATTTGAATTT 601
QY      161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db      602 GGAAGGCTCTTACTTGGGCAATATTTCTCTCTGTTCTCTGATAGCTGGAATCATC 661
QY      181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db      662 CTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTACATGATGCTTACCAAGCC 721
QY      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlsValIleSerGlu 220
Db      722 CAACCTTTTGGCACAAGAGCTCTCCAAAGCTGTCAACTCCCAAGTCAAGAGTGAG 781
QY      221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db      782 TTCAATTCTTACAGCTGACAGGGTATGTG 811

RESULT 12
US-10-063-513-79
; Sequence 79, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

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; APPLICANT: Gueney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; PRIORITY FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-79

Alignment Scores:
Pred. No.:      9,176-218      Length:      1475
Score:          230.00         Matches:      230
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    100.00%        Indels:      0
DB:             14             Gaps:        0

US-09-787-677a-3 (1-230) x US-10-063-513-79 (1-1475)

QY      1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db      122 ATGGCCCTCTTGCCCTCCCACTGTGGGCTACATCTTAGGCCCTTCTGGGGCTTTTGCGC 181
QY      21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerSerTyrValGlyAlaSerIle 40
Db      182 ACACGTGTTGCCATGCTGCTCCCACTGGAACCAAGTTCTTATGTCGGTCCAGCATTT 241
QY      41 ValThrAlaValGlyPheSerIleGlyLeuTyrPheGlyCysAlaThrHisSerThrGly 60
Db      242 GTGACAGCAGTTGGCTTCTCCAAAGGCTCTGATGGAATGTCCACACAGCAGCAGC 301
QY      61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db      302 ATACCCAGGTGACATCTATAGCACCCCTTCTGGGCTGCGCGTGACATCCAGGCTGCC 361
QY      81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValAl 100
Db      362 CAGGCCATGATGGAGCATCATCAGCATCTCTCTCCCTGCGCTCATATCTCTGTGTG 421
QY      101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
Db      422 GGCATGAGATGACAGCTTCTCCAGGAATCCGAGCAAAAGACAGATGGCGGTAGCA 481
QY      121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleTyrAsnLeu 140
Db      482 GGTGGATCTTTTTCATCTTGGAGGCTCTCTGGGATTCATCTCTGTGCTCGGAATCTT 541
QY      141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetCysPheGluIle 160
Db      542 CATGGATCTCTACGGGACTTCTACTCACACTGTGCTGACACAGCAAGAAATTTGAATTT 601
QY      161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db      602 GGAAGGCTCTTACTTGGGCAATATTTCTCTCTGTTCTCTGATAGCTGGAATCATC 661
QY      181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db      662 CTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTACATGATGCTTACCAAGCC 721
QY      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlsValIleSerGlu 220
Db      722 CAACCTTTTGGCACAAGAGCTCTCCAAAGCTGTCAACTCCCAAGTCAAGAGTGAG 781
QY      221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db      782 TTCAATTCTTACAGCTGACAGGGTATGTG 811
```

```
RESULT 13
US-10-063-515-79
; Sequence 79, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-515-79

Alignment Scores:
Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 14

US-09-787-677a-3 (1-230) x US-10-063-515-79 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGly 20
Db 122 ATGGCTCTCTGGCTCCCAACTGTGGCTACATCTTAGGCTTGGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValAlaSerIle 40
Db 182 ACCTGCTGTGCCATGCTGCTCCCAAGTGAAGAAACAAGTTCTTAATGCTGTCAGCATT 241
QY 41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 242 GTACACGACGCTTGGCTTCTCCAGGGCTCTGATGGAATGTGCCACACACAGCAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCACAGGTGACATCTATACACACCTTCTGGGCTGCGCGGTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 362 CAGGCCATGATGTGTGATCATCACTGCAATCTCTCCCTGCGCTGCAATATCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
Db 422 GGCATAGATGCACAGTCTTCTCCAGAGATCCCGAGCCAAAGACAGAGTGGCGGTAGCA 481
QY 121 GlyGlyValAlaPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
Db 482 GGTGGAGTCTTTTCACTCTTGGAGGCTCTGGGATTCATTCCTGTGCTGGAACTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
Db 542 CATGGATCTTACGGAGCTTCTACTCACTGCTGCTTCAAGCATGAATAATTGAGATT 601
QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
Db 602 GGAGAGGCTTTTACTTGGGCAATTATTTCTTCCCTGTTCTCCGTAGTGCAGATCATC 661
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QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCCTGCTTCTCCGCTCATCCAGAGAAATGCTCCAACTACATGATGCTTACCAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db 722 CAACCTTGTCCCAAGAGAGCTCTCCAGGCTGTGTCACCTCCCAAAAGTCAGAGTGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCATTTCTTACAGCTGACAGGATATGTG 811

RESULT 14
US-10-063-512-79
; Sequence 79, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-79

Alignment Scores:
Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 14

US-09-787-677a-3 (1-230) x US-10-063-512-79 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGly 20
Db 122 ATGGCTCTCTGGCTCCCAACTGTGGCTACATCTTAGGCTTGGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValAlaSerIle 40
Db 182 ACCTGCTGTGCCATGCTGCTCCCAAGTGAAGAAACAAGTTCTTAATGCTGTCAGCATT 241
QY 41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 242 GTACACGACGCTTGGCTTCTCCAGGGCTCTGATGGAATGTGCCACACACAGCAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCACAGGTGACATCTATACACACCTTCTGGGCTGCGCGGTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 362 CAGGCCATGATGTGTGATCATCACTGCAATCTCTCCCTGCGCTGCAATATCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
Db 422 GGCATAGATGCACAGTCTTCTCCAGAGATCCCGAGCCAAAGACAGAGTGGCGGTAGCA 481
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QY 121 G1YGLVAlaPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTripaanLeu 140
DB 482 GGTGGAGCTCTTTTTCATCTTGAGGCTCTCGGAGATTCTCTGTGGCTGGAAATCTT 541
QY 141 H1G1Y11eLeuArGaPheTYrSerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CAGGAGATCTTACGGGACTTCTACTCACACTGGTGTGCTGACAGCAATTTGAATTT 601
QY 161 G1YGLuAlaLeuTYrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 602 GGAGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTTCTCCCTGATAGCTGGAAATCATC 661
QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAntTYrTYrAspAlaTYrGlnAla 200
DB 662 CTCTGCTTTTCCCTGCTCATCTCCAGAGAAATCGCTCAACTACTAGATGCTTACCAAGCC 721
QY 201 G1nProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
DB 722 CAACCTCTTCCACAGAGACTCTCCAAAGCCTGTGTACCTCCCAAGTCAGAGATGAG 781
QY 221 PheAsnSerTYrSerLeuThrgIYrVal 230
DB 782 TTCATTCCTACAGCTGACAGGCTATGTG 811
RESULT 15
US-10-121-049-491
Sequence 491, Application US/10121049
Publication No. US2003002239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
Pilot Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 491
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-121-049-491
Alignment Scores:
Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-09-787-677a-3 (1-230) x US-10-121-049-491 (1-1475)
QY 1 Meta1aSerLeuGlyLeuGlnLeuValGlyTYrIleLeuGlyLeuLeuGlyLeuLeuGly 20
DB 122 ATGGCCCTCTTGCCCTCAACTGTGGGCTACATCTTCCAGGCTTCTGGGGCTTTTGGGC 181

QY 21 ThrLeuValAlaMetLeuLeuProSerTriPheThrsSerTYrValGlyAlaSerIle 40
DB 182 ACATGCTTCCATCTGCTGCTCCCACTGGAGAAACAAAGTTCTTAATGCTGCTGCAGATT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTriPheGluCysAlaThrHisSerThrgIy 60
DB 242 GTGACAGCAATTTGGCTTCTCAAGGGCTCTGGATGGAATGTGCAACACAGACAGGAGCC 301
QY 61 IleThrgInCysAspIleTYrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
DB 302 ATCACCAGAGTGAACATCTATACACCTTCTGGGCTGTGCTGCAATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
DB 422 GGATGAGATGACAGATCTTCTGCAAGAAATCCGAGCAAAAGACAGATGGGGGTAGCA 481
QY 121 G1YGLVAlaPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTripaanLeu 140
DB 482 GGTGGAGCTCTTTTTCATCTTGAGGCTCTCGGAGATTCTCTGTGGCTGGAAATCTT 541
QY 141 H1G1Y11eLeuArGaPheTYrSerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CAGGAGATCTTACGGGACTTCTACTCACACTGGTGTGCTGACAGCAATTTGAATTT 601
QY 161 G1YGLuAlaLeuTYrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 602 GGAGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTTCTCCCTGATAGCTGGAAATCATC 661
QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAntTYrTYrAspAlaTYrGlnAla 200
DB 662 CTCTGCTTTTCCCTGCTCATCTCCAGAGAAATCGCTCAACTACTAGATGCTTACCAAGCC 721
QY 201 G1nProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
DB 722 CAACCTCTTCCACAGAGACTCTCCAAAGCCTGTGTACCTCCCAAGTCAGAGATGAG 781
QY 221 PheAsnSerTYrSerLeuThrgIYrVal 230
DB 782 TTCATTCCTACAGCTGACAGGCTATGTG 811

Search completed: December 20, 2004, 21:38:46
Job time : 551 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 17:55:02 ; Search time 3199 Seconds
(without alignments)
2619.924 Million cell updates/sec

Title: US-09-787-677A-3
Perfect score: 230
Sequence: 1 MASLSGLVGYITGLLGLG.....PGQPKVKSFRNSYSLTYV 230

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Word size: 1

Total number of hits satisfying chosen parameters: 65644297

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-Q/cgml 1/USPTO.spool/US09787677/runat 20122004 132817 19771/app query.fasta_1.391
-DB=BSF -OFT=fastap -SUPFIX=oli.rst -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_hic: *
4: gb_esc3: *
5: gb_esc4: *
6: gb_esc5: *
7: gb_esc6: *
8: gb_gsa1: *
9: gb_gsa2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	100.0	693	9 AY400251	AY400251 Homo sapi
2	208	90.4	693	9 AY400252	AY400252 Pan trogl
3	195	84.8	680	2 BR304667	BR304667 601105783
4	191	83.0	822	4 BG386074	BG386074 602455248
5	179	77.8	728	4 BG325755	BG325755 602424466
6	171	74.3	650	7 CR546700	CR546700 DKF2P470L
7	171	74.3	652	7 CR628947	CR628947 DKF2P469L
8	155	67.4	978	4 BG164062	BG164062 602341087
9	153	66.5	494	4 BG385562	BG385562 602453858

10	124	53.9	945	2 BE513091	BE513091 601171545
11	122	53.0	570	7 CR628828	CR628828 DKF2P469B
12	119	51.7	758	6 CB999779	CB999779 AGENCOURT
13	113	49.1	459	6 CA389170	CA389170 cs06d06.y
14	111	48.3	421	7 CR554772	CR554772 DKF2P469E
15	110	47.8	560	1 AI953481	AI953481 wg29b02.x
16	79	34.3	643	4 BG328625	BG328625 602427889
17	74	32.2	359	7 T86266	T86266 y084h07.r1
18	64	27.8	866	2 BF032123	BF032123 601559727
19	59	25.7	655	7 CK975368	CK975368 4106492 B
20	59	25.7	761	5 BP445902	BP445902 BP445902
21	58	25.2	403	1 AI116661	AI116661 ue28a02.y
22	58	25.2	437	6 CB790981	CB790981 AGENCOURT
23	58	25.2	458	2 BF789570	BF789570 602103665
24	58	25.2	470	7 CK322258	CK322258 K0843E08-
25	58	25.2	496	6 CA885318	CA885318 B0117E04-
26	58	25.2	520	1 A1746647	A1746647 u101904.y
27	58	25.2	564	6 BY705200	BY705200 BY705200
28	58	25.2	593	1 A1789119	A1789119 u51c01.y
29	58	25.2	648	7 CK390708	CK390708 K0822D03-
30	58	25.2	659	1 A1789490	A1789490 UK99h03.y
31	58	25.2	693	9 AY400253	AY400253 Mus muscu
32	58	25.2	704	4 B1330754	B1330754 602982419
33	58	25.2	727	4 B1101652	B1101652 602887470
34	58	25.2	736	5 BM951102	BM951102 UT-M-EHO-
35	58	25.2	738	6 CA467958	CA467958 AGENCOURT
36	58	25.2	750	2 AW475316	AW475316 un04d02.y
37	58	25.2	752	6 CB952500	CB952500 AGENCOURT
38	58	25.2	754	7 CK129571	CK129571 AGENCOURT
39	58	25.2	762	7 CK021120	CK021120 AGENCOURT
40	58	25.2	774	7 CK031415	CK031415 AGENCOURT
41	58	25.2	777	4 B1102100	B1102100 602887847
42	58	25.2	786	8 B2215522	B2215522 CH230-416
43	58	25.2	787	2 BF781962	BF781962 602106220
44	58	25.2	818	6 CA469360	CA469360 AGENCOURT
45	58	25.2	836	6 CA492032	CA492032 AGENCOURT

ALIGNMENTS

RESULT 1	AY400251	693 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY400251				
DEFINITION	Homo sapiens CLDN2 gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	AY400251				
VERSION	AY400251.1	GI:39756240			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 693) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smirsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 693) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smirsky,J.J., Adams,M.D. and Cargill,M.				
AUTHORS	Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.				
TITLE	Location/Qualifiers				
COMMENT	1. .693				
FEATURES	source				

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/mol_type="genomic DNA"
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/gene="CLDN2"
/locus_tag="HCM0495"

ORIGIN

Alignment Scores:
Pred. No.: 4.32e-214 Length: 693
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-787-677A-3 (1-230) x AY400251 (1-693)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly 20
Db 1 ATGGCTCTCTTGGCTCCCACTTGTGGCTACCTCCTAGGCTTCTGGGCTTTTGGGC 60
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValGlyAlaSerIle 40
Db 61 ACACTGGTTCGACAGTCTGCTCCAGCTGGAAAACAAGTTCTTATGTCGGTCCAGCATT 120
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
Db 121 GTGACAGACAGTTGGCTTCTCCAGAGGCTCTGAGATGATGTGCACACACAGCAGGC 180
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db 181 ATCACCAGTGTACATCTATAGCACTTGTGGCTTGGCCCTGACATCCAGGCTGCC 240
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 241 CAGGCCATGATGGGATCATCAGTCAATCTCTCCCTGGCTGCATTAATCTGTGGTG 300
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
Db 301 GGCATGATGATGACAGTCTTGTCCAGAAATCCGAGCAGAAAGACAGATGGCGGTAGCA 360
QY 121 GlyValAlaPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaThrAspLeu 140
Db 361 GGTGGATCTTTTTCATCTTGGAGGCTCTGGGATTCATCTCTGTGGCTGGAATCTT 420
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 421 CATGGATCTTACGGGACTTCTACTCACTGGTGGCTGACAGCATGAATTTGAGATT 480
QY 161 GlyValAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 481 GGAAGGCTCTTAACTTGGCATTAATTTCTTCCCTGTTCTCCGATAGCTGGAATCATC 540
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 541 CTCTGCTTTCTCTCTCATCCCAAGAAATGCTCCCAACTACTGATGCTTACCAAGCC 600
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValIleSerGlu 220
Db 601 CAACCTCTTGCCACAAGAGCTTCCAAAGGCTGTCAACTCCCAAGTCAAGAGGTAG 660
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 661 TTCAATTCCTACACCTGACAGGGGTATGTG 690

RESULT 2
AY400252 693 bp DNA linear GSS 15-DEC-2003
LOCUS Pan troglodytes CLDN2 gene, VIRUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY400252
VERSION AY400252.1 GI:39756241

KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
AUTHORS 1 (bases 1 to 693)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Givello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene clusters
Science 302 (5652), 1960-1963 (2003)
JOURNAL PUBMED 14671302
REFERENCE 2 (bases 1 to 693)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Givello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source 1..693
gene /organism="Pan troglodytes"
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ORIGIN

Alignment Scores:
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Score: 208.00 Matches: 208
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.43% Indels: 0
DB: Gaps: 0

US-09-787-677A-3 (1-230) x AY400252 (1-693)

QY 23 ValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValGlyAlaSerIleValThr 42
Db 67 GTTGGCATGCTGCTCCCACTGGAACAAGTTCTTACGTCGGTGCAGCATTTGACA 126
QY 43 AlaValGlyPheSerLysGlyLeuTyrMetGluCysAlaThrHisSerThrGlyIleThr 62
Db 127 GCACTTGGCTTCTCCAGAGGCTCTGATGGAATGTCCACACACACAGGATCACC 186
QY 63 GlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAlaGlnAla 82
Db 187 CAGTGTACATCTATACACACCTTCTGGGCTGCCCTGACATCCAGGCTGCCAGGCC 246
QY 83 MetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValIleGlyMet 102
Db 247 ATGATGTGTACATCCATGCAATCTCTCCCTGGCTGCAATTAATCTGTGGTGGCATG 306
QY 103 ArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaAlaGlyGly 122
Db 307 AGATGCACAGCTTCTTCCAGGAATCCGAGCCAAACAAGAGGGCGGTAGCAGGTGGA 366
QY 123 ValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaThrAsnLeuHisGly 142
Db 367 GTCTTTTCATCTTGGAGGCTCTCGGATTCATCTCTGTGCTGGAAATCTTCATGGG 426
QY 143 IleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIleGlyGlu 162
Db 427 ATCTTACGGGACCTTCTACTACCACTGTGCTGCACGATGAATTTGAGATTGGAGAG 486
QY 163 AlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIleLeuCys 182

Db	487	GCTTTTACTTGGGCATTTATTTCTTCCCTGTTCTTCCCGAAGCTGGAATATCTCTGC	546
Qy	183	PheserCysserSergInatAgsnarSeraantYrYraaPaIaYrGInaIaGInPro	202
Db	547	TTTTCTGTCATCCACAGAAATCGCTCAACTACTACGATGCTCAACCAAGCCAACT	606
Qy	203	LeuAaIhAraaSerSerProAqProGInProPolysVallybSerGluPheasn	222
Db	607	CTTGCCACACAGAGACTCTCCAGGCGTGGTCAACCTCCAAAGTCMAAGTAGATTCAAT	666
Qy	223	SerTySerLeuThrInGlyrYVal	230
Db	667	TCTACAGCCTGACAGGGTATGTC	690
RESULT 3			
LOCUS	BE304667	680 bp	mRNA linear EST 13-JUL-2000
DEFINITION	601105783P1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:2988309 5',		
ACCESSION	BE304667		
VERSION	BE304667.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 680) NIH-MGC http://mgs.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMU, at: image.llnl.gov Plate: LUCM77 row: f column: 22 High quality sequence start: 27 High quality sequence stop: 680. Location/Qualifiers 1. .680 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:2988309" /tissue_type="adenocarcinoma cell line" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 15" /note="Organ: colon; Vector: POTB7; Site 1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5'- adapter: GGCACTAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"		
FEATURES			
Source			
ALIGNMENT SCORES:			
Prod. NO.:	6,89e-180	Length:	680
Score:	195.00	Matches:	195
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	84.78%	Indels:	0
DB:	2	Gaps:	0
US-09-787-677A-3 (1-230) x BE304667 (1-680)			
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D	b		38	GTCGGTCCAGACANTGTGAOCAGCAGTTGGCTTCCCAAGGAGCCCTCGATGCAGTAATGTGCC	97
Oy			56	ThHiseSerThrglyllethrInCyAspIleTySerThrLeuleuGlyLeuProAla	75
D	b		98	ACAACAGACACAGGCATCACCCAGTGATCATATTATGTGACCCTTCCTGGGCGCTCCGCT	157
Oy			76	AspIleGlnIlaIagIlnalameMetValThrSerSerAlaIleSerSerLeuAlaCys	95
D	b		158	GACATCCAGGCGTCCCAGGCGCATGATGTATGTACATCCAGTGCATCTCCCTGGCTGC	217
Oy			96	IleIleSerValValGlyMetArgCysThrValPheCysGlnGluSerAArgAlaLysAsp	115
D	b		218	ATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCCTCCAGAAATCCCAAGCCAAAAGAC	277
Oy			116	ArgValAlaValAlaIagIlylvalPhePheIleLeuGlyGlyLeuGlyPheIlePro	135
D	b		278	AGA GTGCGCGGTAGACAGGTGAGTCTTTTTCATCTTCGTGAGAGCCCTCTGGGATTCATTCT	337
Oy			136	ValAlaIarPhaenueHIsGlyIleLeuArgAspPheTySerProLeuValProAspSer	155
D	b		338	GTTGCCCCGGAATCTTCATGGATCTCAAGGACTTCACTCACCACTGTGCTCGAACGC	397
Oy			156	MethYspHeGluIleGlyGlyAlaLeuTyLeuGlyIleIleSerSerLeuPheSerLeu	175
D	b		398	ATGAATTTTGAGATGTGAGAGGCTCTTTACTTGGGCATTTATTTCTTCCTTCCTG	457
Oy			176	IleAlaGlyIleIleLeuCyPhePheSerCysSerSerGlnArgAsnAArgSerAsnTyTr	195
D	b		458	ATACTGGAATCATCTCTGCTTTTCTGCTGATCCAGAGAAATCGCTCCAATCTAC	517
Oy			196	AspAlaTyTrGlnAlaGlnProLeuAlaThrArgSerSerProAlaGProGlyGlnProPro	215
D	b		518	GATGCCATCAACAGGCCAACCTCTTGCCACAAGAGGCTCTCCAAAGCCTGTGTCACTCCC	577
Oy			216	LysValLysSerGluPheAsnSerTySerLeuThrGlyTyTrVal	230
D	b		578	AAGSTCAAGATGATGTTCAATTCTCAAGCCTGACAGAGGATGTG	622
RESULT 4					
LOCUS	BG386074		822 bp	mRNA	linear EST 12-MAR-2001
DEFINITION	60245524F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4583675 5,				
ACCESSION	BG386074				
VERSION	BG386074.1		GI:13279520		
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
TITLE	1 (bases 1 to 822)				
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabds@email.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLB) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLB at: http://image.lnlb.nih.gov Plate: LECMI307 row: P column: 12 High quality sequence stop: 746. Location/Qualifiers 1..822 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4583675" /tissue_type="adenocarcinoma cell line" /lab_host="DH10B (phage-resistant)"				
FEATURES	source				

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 /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies) "

ORIGIN

Alignment Scores:

Pred. No.:	6 79e-176	Length:	822
Score:	191.00	Matches:	191
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	83.04%	Indels:	0
DB:	4	Gaps:	0

US-09-787-677a-3 (1-230) x BG386074 (1-822)

QY 1 MetAlaSerLeuGlnLeuValGlyTyrIleuGlyLeuLeuGly 20
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 DB 187 ACACTGGTTCAGAGCTGCTCCAGCTGGAACCAAGTTTATGTCGGGCGACGATTT 246
 QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
 DB 247 GTGACAGCAATGGCTTCTCCAAAGGCTCTCGATGGAATGTCACACACAGACAGGC 306
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
 DB 307 ATCACCAGTGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCAGGCTGCC 366
 QY 81 GlAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 367 CAGGCCATGATGGAGCAATCCAGTCAATCTCCCTCGGCTCATTTATCTGTGGTG 426
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIlyAspArgValAlaValAla 120
 DB 427 GGCATGATGATGACAGCTTCTGCGCAGGAATCCGAGCAAGAGTGGCGTGCA 486
 QY 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTrpAsnLeu 140
 DB 487 GGTGAGCTCTTTTCATCTTGGAGGCTCTCGGATTCATCTCTGTGCTGGAATCTT 546
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 DB 547 CATGGATCTCAGCGACTTCTACTCACCTGAGTGGCTGACACAGAAATTTGAGATT 606
 QY 161 GlyIleValLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 DB 607 GGAGAGGCTCTTTCATCTTGGGATTTCTTCCCTGTTCTCGATGAGTGGATATC 666
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArg 191
 DB 667 CTCTGCTTTCTCTGCTCATCCAGAAATCGT 699
 RESULT 5
 BG325755 728 bp mRNA linear EST 27-FEB-2001
 LOCUS BG325755 602424466F1 NIH MGC 14 Homo sapiens cDNA clone IMAGE:4562273 5',
 DEFINITION mRNA sequence.
 accession BG325755
 version BG325755.1 GI:13132179
 keywords EST.
 source Homo sapiens (human)
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 728)
 AUTHORS NIH-MGC <http://imgc.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 plate: LICM274 row: d column: 18
 High quality sequence stop: 708.
 Location/Qualifiers

FEATURES

source

1. 728
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4562273"
 /tissue_type="renal cell adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH MGC 14"
 /note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies) ."

ORIGIN

Alignment Scores:

Pred. No.:	3.22e-164	Length:	728
Score:	179.00	Matches:	196
Percent Similarity:	99.49%	Conservative:	0
Best Local Similarity:	99.49%	Mismatches:	1
Query Match:	77.83%	Indels:	1
DB:	4	Gaps:	0

US-09-787-677a-3 (1-230) x BG325755 (1-728)

QY 1 MetAlaSerLeuGlnLeuValGlyTyrIleuGlyLeuLeuGly 20
 DB 30 ATGGCTCTTGGCTCCAACTGTGGCTACATCTAGGCTTGGGCTTTGGGC 88
 QY 21 ThrLeuValAlaMetLeuProSerTrpLysSerSerTyrValGlyAlaSerIle 40
 DB 89 ACACTGGTTCAGAGCTGCTCCAGCTGGAACCAAGTTTATGTCGGGCGACGATTT 148
 QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
 DB 149 GTGACAGCAATGGCTTCTCCAAAGGCTCTCGATGGAATGTCACACACAGCAGGC 208
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
 DB 209 ATCACCAGTGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCAGGCTGCC 268
 QY 81 GlAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 269 CAGGCCATGATGGAGCAATCCAGTCAATCTCCCTGCGCTGATTTATCTGTGGTG 328
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIlyAspArgValAlaValAla 120
 DB 329 GGCATGATGATGACAGCTTCTGCGCAGGAATCCGAGCAAGAGTGGCGTGCA 388
 QY 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTrpAsnLeu 140
 DB 389 GGTGAGCTCTTTTCATCTTGGAGGCTCTCGGATTCATCTCTGTGCTGGAATCTT 448
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160

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Db      449 CATGGATCTTACGGAGCTTCTACTCACCAGCTGGCTTACACCAAGAAATTTGAGATT 508
      |||
Qy      161 G1yG1uAlaLeuYrLeuG1y1le1leSerSerLeuPheSerLeu1leAlaG1y1le1le 180
      |||
Db      509 GGAGAGCTCTTACTGAGGATATTCTTCCCTGTTCTCCCGATAGCTGGAAATATC 568
      |||
Qy      181 LeuCyPheSerCySerSerG1nArGaBnArGaSerAntYrYrAaPa1a 197
      |||
Db      569 CTCTGCTTTCTCTGCTCATCCAGAGAAATGCTCCAACTACTACGATGCT 619
      |||

RESULT 6
CR546700      650 bp      mRNA      linear      EST 07-JUL-2004
DEFINITION    DKFZp470L1824_r1.470 (synonym: pliv1) Pongo pygmaeus cDNA clone
ACCESSION     CR546700
VERSION       CR546700.1 GI:49899227
KEYWORDS      EST.
SOURCE        Pongo pygmaeus (orangutan)
ORGANISM      Pongo pygmaeus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
1 (bases 1 to 650)
Wamburt,R., Heubner,D., Mewes,H.W., Weill,B., Amid,C., Oeanger,A.,
Fobo,G., Han,M. and Wiemann,S.
Pongo pygmaeus mRNA (Wamburt,R., Heubner,D., Mewes,H.W., et al.)
Unpublished (2004)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKF2);
Email s.wiemann@dkfz-heidelberg.de; sequenced by Agowa
(Berlin/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp470L1824) is available at
the RZPD in Berlin. Please contact the RZPD: Ressourcentrum,
Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email:
sequencing@rzd.de Further information about the clone and the
sequencing project is available at
http://mips.gsf.de/projects/cdna/.
location/Qualifiers
1..650
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp470L1824"
/tissue_type="liver"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1b="470 (synonym: pliv1)"
/note="Vector: pSport1_Sfi1, Site_1: SfiIA, Site_2: SfiIB"

ORIGIN
Alignment Scores:
Pred. No.:      1.89e-156      Length:      650
Score:          171.00      Matches:      171
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    74.35%      Indels:      0
DB:             7      Gaps:      0

US-09-787-677A-3 (1-230) x CR546700 (1-650)

Qy      1 MetAlaSerLeuG1yLeuG1nLeuValG1Yr1leleuG1yLeuG1yLeuG1y 20
      |||
Db      137 ATGGCTCTCTTGGCTCCCAACTGTGGGCTACATCTTACGGCTTTGGGGCTTTGGGC 196
      |||
Qy      21 ThrLeuValAlaMetLeuLeuProSerTrpLyArThrSerSerYrValG1yAlaSer1le 40
      |||
Db      197 ACACGTGTCATGCTGCTCCAGCTGGAAACAAATTCTTACGTCGGGCGACGATTT 256
      |||
Qy      41 ValThrAlaValG1yPheSerLyG1yLeuTrpMetG1nCyAlaThrAlaSerThG1y 60
      |||

```

```

Db      257 GTGACACAGATGGCTCTTCTCAAGAGGCTTGGATGGAGTGTGCCACACAGACAGCT 316
      |||
Qy      61 IleThrG1nCyAsp1leYrSerTrhLeuG1yLeuProAlaAsp1leG1nAla1a 80
      |||
Db      317 ATCACCCAGATGATACATCTATACACACCTTCTGGGCTGCGCGGTGATCCAGGCTGCC 376
      |||
Qy      81 G1nAlaMetMetValThrSerSerAla1leSerSerLeuAlaCyAlle1leSerVal1a 100
      |||
Db      377 CAGGCCATGATGTGATCATCATCATGCAATCTCTCCCTGCGCTGCATTAATCTGTGGTG 436
      |||
Qy      101 G1yMetArGySerThrValPheCyG1nG1nUserArG1a1yAspArG1a1aVal1a 120
      |||
Db      437 GGCAATGATGATCACAGCTTCTCCAGAGAAATCCAGACCAAGACAGATGGCGATGCA 496
      |||
Qy      121 G1yG1yAlaPhePhe1leleuG1yLeuG1yPhe1leProValAla1rPaSnLeu 140
      |||
Db      497 GGTGAGCTCTTTTTCATCTTGGAGAGGCTCTGGGCTTCAATTCCTGTGCTGGAACTT 556
      |||
Qy      141 HisG1y1leleuArGaPheTySerProLeuValProAspSerMetLySpheG1u1le 160
      |||
Db      557 CATGGATCTTACGGAGCTTCTACTCACCAGCTGGCTGACAGCATGAATTTGAGATT 616
      |||
Qy      161 G1yG1uAlaLeuYrLeuG1y1le1leSerSer 171
      |||
Db      617 GGAGAGCTCTTACTTGGGCAATTATTTCTTCC 649
      |||

RESULT 7
CR628947      652 bp      mRNA      linear      EST 11-AUG-2004
DEFINITION    DKFZp469L0623_r1.469 (synonym: pkid1) Pongo pygmaeus cDNA clone
ACCESSION     CR628947
VERSION       CR628947.1 GI:51125027
KEYWORDS      EST.
SOURCE        Pongo pygmaeus (orangutan)
ORGANISM      Pongo pygmaeus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
1 (bases 1 to 652)
Ansoerge,W., Krieger,S., Regiert,T., Rittmuller,C., Schwager,B.,
Mewes,H.W., Weill,B., Amid,C., Oeanger,A., Fobo,G., Han,M. and
Wiemann,S.
Pongo pygmaeus mRNA (Ansoerge,W., Krieger,S., Regiert,T., et al.)
Unpublished (2004)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKF2);
Email s.wiemann@dkfz-heidelberg.de; r1in, Germany. Please contact
RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/c1.cgi?cloneID=DKFZp469L0623
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
location/Qualifiers
1..652
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469L0623"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1b="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi1, Site_1: SfiIA, Site_2: SfiIB"

ORIGIN
Alignment Scores:
Pred. No.:      1.9e-156      Length:      652
Score:          171.00      Matches:      171
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0

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Query Match: 74.35% Indel: 0
DB: 7 Gaps: 0
US-09-787-677a-3 (1-230) x CR628947 (1-652)

Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db 138 ATGGCCCTCTTGCCCTCCCAACTGTGGGGTACATCTTAGGCTCTTGGGGCTTTGGGC 197

Qy 21 ThrLeuValAlaMetLeuLeuProSerTTrpLysThrSerSerTyrValGlyAlaSerIle 40
Db 198 ACACGTGGTGCATGCTGCTCCCGAGCAAAAGATTCTTACGTGGGTGCAGCATT 257

Qy 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
Db 258 GTGACAGCAGTGTGCTCTCCAGGGCTCTGGATGGAGTGTGCACACACAGCAGGT 317

Qy 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 318 ATCACCAGGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGCTGCC 377

Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 378 CAGGCCATGATGGATCATCCAGATCATCTCTCCCTGGCTGCATTATCTGTGTG 437

Qy 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaLysAspArgValAlaValAla 120
Db 438 GGCACTGATGATGACATCTTTCGACAGAAATCCGAGCCAAAGACAGATGGCGGTGCA 497

Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
Db 498 GGTGGATCTTTTTCATCTTGGAGGCTCTGGGCTTCACTCTGTGGCTGGAATCTT 557

Qy 141 HisGlyIleLeuAlaGlyAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 558 CATGGGATCTTACCGGACTTCTACTCACACTGTGCTGCACACATGAATTTTGAGATT 617

Qy 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSer 171
Db 618 GGAGAGCTCTTTTACTTGGGCAATTATTTCTTCC 650

RESULT 8
LOCUS BG164062 978 bp mRNA linear EST 06-FEB-2001
DEFINITION 60234108F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4449212 5',
mRNA sequence.
ACCESSION BG164062
VERSION BG164062.1 GI:12670765
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 978)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-rc@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM10232 row: m column: 21
High quality sequence stop: 689.
Location/Qualifiers
1..978
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

Alignment Scores:
Pred. No.: 1.25e-140 Length: 978
Score: 155.00 Matches: 185
Percent Similarity: 98.93% Conservative: 0
Best Local Similarity: 98.93% Mismatches: 1
Query Match: 67.39% Indels: 2
DB: 4 Gaps: 0
US-09-787-677a-3 (1-230) x BG164062 (1-978)

Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db 25 ATGGCCCTCTTGCCCTCCCAACTGTGGGGTACATCTTAGGCTCTTGGGGCT-TTGGGC 83

Qy 21 ThrLeuValAlaMetLeuLeuProSerTTrpLysThrSerSerTyrValGlyAlaSerIle 40
Db 84 ACACGTGGTGCATGCTGCTCCCGAGCAAAAGATTCTTATGCGGTGCAGCATT 143

Qy 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
Db 144 GTGACAGCAGTGTGCTCTCCAGGGCTCTGGATGGATGTGCCACACACACAGC 203

Qy 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 204 ATCACCAGGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGCTGCC 263

Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 264 CAGGCCATGATGGATCATCCAGATCATCTCTCCCTGGCTGCATTATCTGTGTG 323

Qy 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaLysAspArgValAlaValAla 120
Db 324 GGCACTGATGATGACATCTTTCGACAGAAATCCGAGCCAAAGACAGATGGCGGTGCA 383

Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
Db 384 GGTGGATCTTTTTCATCTTGGAGGCTCTGGGATTCATCTCTGTGGCTGGAATCTT 443

Qy 141 HisGlyIleLeuAlaGlyAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 444 CATGGGATCTTACCGGACTTCTACTCACACTGTGCTGCACACATGAATTTTGAGATT 503

Qy 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPhePheSerLeuIleAlaGlyIle 180
Db 504 GGAGAGCTCTTTTACTTGGGCAATTATTTCTCTGTTCTCCCTGATAGCTGGAATCAT 563

Qy 180 eLeuCysPheSerCysSer 186
Db 564 CTTCTGCTTTCTGTGCTCA 582

RESULT 9
LOCUS BG385562 494 bp mRNA linear EST 12-MAR-2001
DEFINITION 602453856F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4582214 5',
mRNA sequence.
ACCESSION BG385562
VERSION BG385562.1 GI:13278350
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 494)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LNCM304 row: C column: 15
 High quality sequence stop: 493.
 Location/Qualifiers

FEATURES

source

1. 494
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4582214"
 /issue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC_15"
 /note="Organ: colon; Vector: pOT87; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Alignment Scores:

Pred. No.: 5 62e-139 Length: 494
 Score: 153.00 Matches: 153
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 66.52% Indels: 0
 DB: 4 Gaps: 0

US-09-787-677a-3 (1-230) x BG385562 (1-494)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
 DB 35 ATGGCCTCTTGGCTCCCACTTGTGGCTACATCTTAGGCTTGTGGGCTTTGGGC 94
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLyThrSerSerTrpValGlyAlaSerIle 40
 DB 95 ACACGTGGTCCATGCTGCTCCCACTGAGAAACAAGTTCTTAATGCGGTGCACGACTT 154
 QY 41 ValThrAlaValGlyPheSerLySGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
 DB 155 GTACACGACATTTGGCTTCTCCAAAGGCTCTTGATGAAATGTGCCACACACAGCAGGC 214
 QY 61 IleThrGlnCysAspIleIleTrpSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
 DB 215 ATACACCAAGTGAATCTAATAGACACCTTCTGGGCTGCGCGGTGACATCCAGGCTGCC 274
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 275 CAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 334
 QY 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaIleValAspValAlaValAla 120
 DB 335 GGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 394
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaATPAsnLeu 140
 DB 395 GGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 454
 QY 141 HisGlyIleLeuArgAspPheTrpSerProLeuValPro 153

DB 455 CATGGATCTTACGGACTTCTTACTACACATGCTGCT 493

RESULT 10
 BE513091 945 bp mRNA linear EST 07-AUG-2000
 LOCUS 601171545F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3545171 5',
 DEFINITION
 mRNA sequence.
 ACCESSION BE513091
 VERSION BE513091.1 GI:9720302
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 945)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LNCM241 row: 1 column: 12
 High quality sequence start: 36
 High quality sequence stop: 782.
 Location/Qualifiers

FEATURES

source

1. 945
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3545171"
 /issue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC_15"
 /note="Organ: colon; Vector: pOT87; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Alignment Scores:

Pred. No.: 2.42e-110 Length: 945
 Score: 124.00 Matches: 158
 Percent Similarity: 99.37% Conservative: 0
 Best Local Similarity: 99.37% Mismatches: 1
 Query Match: 53.91% Indels: 1
 DB: 2 Gaps: 0

US-09-787-677a-3 (1-230) x BE513091 (1-945)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
 DB 187 ATGGCCTCTTGGCTCCCACTTGTGGCTACATCTTAGGCTTGTGGGCTTTGGGC 246
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLyThrSerSerTrpValGlyAlaSerIle 40
 DB 247 ACACGTGGTCCATGCTGCTCCCACTGAGAAACAAGTTCTTAATGCGGTGCACGACTT 306
 QY 41 ValThrAlaValGlyPheSerLySGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
 DB 307 GTACACGACATTTGGCTTCTCCAAAGGCTCTTGATGAAATGTGCCACACACAGCAGGC 366
 QY 61 IleThrGlnCysAspIleIleTrpSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80

Db 367 ATCACCAGTGTACATCTAATAGACACCCCTTCTGGGCGCTGCCGTGACATCCAGCTGCC 426
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal1 100
 Db 427 CAGGCCATGATGTGATGATCAGTCAATCTCCCTGGCGCTGATTAATCTCTGTGTG 486
 QY 101 G1MeArGcYsThrValPheCyGInG1uSerArGAlaIysAPaPvAlAlaValAla 120
 Db 487 GGCATGAGATGACAGATCTTCTGCGAGAAATCCGAGCCAAAGACAGATGCGGTAGCA 546
 QY 121 G1YG1YValPhePheIleLeuG1Y1YLeuLeuG1YpHeIleProValAlaIATPAsnLeu 140
 Db 547 GGTGAGATCTT-TTCATCTTGGAGGCTCCTGGATTCATCTCTGTGCTGGAACTT 605
 QY 141 H1G1Y1IleLeuArGApPheTySerProLeuValProAspSerMetIYpHeG1u 159
 Db 606 CATGGATCTTACCGGAGCTTCTACTCACTGCTGCTGACAGATGAATTTGAA 662

RESULT 11
 LOCUS CR628828 570 bp mRNA linear EST 11-AUG-2004
 DEFINITION DKFZp469B1623_r1 469 (synonym: pkidi) Pongo pygmaeus cDNA clone
 CR628828
 VERSION CR628828
 KEYWORDS CR628828.1 GI:51124908
 EST.

SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 1 (bases 1 to 570)
 Ansoerge W., Krieger, S., Regiert, T., Rittmeller, C., Schwager, B., Mewes, H.W., Well, B., Amid, C., Osanger, A., Fobo, G., Han, M., and Wiemann, S.

TITLE Pongo pygmaeus mRNA (Ansoerge, W., Krieger, S., Regiert, T., et al.)
 JOURNAL Unpublished (2004)
 COMMENT Contact: MIPS

MPIS
 This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp469B1623
 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

FEATURES
 Source
 1..570
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp469B1623"
 /issue_type="Kidney"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="469 (synonym: pkidi)"
 /note="Vector: pSPORT1_Sfi; Site_1: SfiIa; Site_2: SfiIb"

ORIGIN

Alignment Scores:
 Pred. No.: 1..36-108 Length: 570
 Score: 122.00 Matches: 122
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 53.04% Indels: 0
 DB: 7 Gaps: 0

US-09-787-677a-3 (1-230) x CR628828 (1-570)

QY 1 MetLaserLeuG1YLeuGlnLeuValG1YTrIleLeuG1YLeuLeuG1YLeuLeuG1Y 20
 Db 146 ATGGCTCTCTTGGCTCCCACTGTGTGGCTTACATCTCAGGCTTCTGGGGCTTTTGGGC 205

QY 21 ThrLeuValAlaMetLeuLeuProSerTrpIYpThrSerSerTyValG1YAlaSerIle 40
 Db 206 ACACTGTTCCATGCTGCTCCCACTGGAAAAACAAGTTCTTAACGCGGTGCAGATT 265
 QY 41 ValThrAlaValG1YPheSerIYg1YLeuTrpMeG1uCyValaThrIleSerThrngly 60
 Db 266 GTACAGACAGATTGGCTTCTCCCAAGGGCTCTGTGATGAGAGTGCACACACACAGGT 325
 QY 61 ILThG1nCyAspIleTySerThrLeuLeuG1YLeuProAlaAspIleGlnAlaAla 80
 Db 326 ATCACCAGTGTACATCTAATACACCTTCTGGGCTGCCCTGACATCCAGGCTGCC 385
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal1 100
 Db 386 CAGGCCATGATGTGATGATCAGTCAATCTCCCTGGCGCTGATTAATCTCTGTGTG 445
 QY 101 G1MeArGcYsThrValPheCyGInG1uSerArGAlaIysAPaPvAlAlaValAla 120
 Db 446 GGCATGAGATGACAGATCTTCTGCGAGAAATCCGAGCCAAAGACAGATGCGGTAGCA 505

RESULT 12
 LOCUS CB999779 758 bp mRNA linear EST 01-MAY-2003
 DEFINITION AGENCOURT_13642925 NIH_MGC_186 Homo sapiens cDNA clone
 CB999779
 VERSION CB999779
 KEYWORDS CB999779.1 GI:30294299
 EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 758)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strauberg, Ph.D.
 Email: c9abs-rc@mail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: NDCM124 row: 1 column: 05
 High quality sequence stop: 592.

FEATURES
 Source

Location/Qualifiers
 1..758
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30322852"
 /lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_186"
 /note="Organ: Pooled-Skin; Vector: pDNR-LIB; Site_1: SfiI (ggcgcctggcgc); Site_2: SfiI (ggcgcctggcgc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a pooled samples of tissues from Skin, meninges, dura mater, pia mater and choroid plexus. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGGCGGAGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.47 kb (range 0.50-4.0 kb). 15/15 clones contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library"

ORIGIN

Alignment Scores:

Pred. No.:	1,496-105	Length:	758
Score:	119.00	Matches:	119
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	51.74%	Indels:	0
DB:	6	Gaps:	0

US-09-787-677A-3 (1-230) x CB999779 (1-758)

```

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTlleLeuGlyLeuLeuGlyLeuLeuGly 20
   |||||
Db 331 ATGGCCCTCTTGGCCCTCCCACTGGGCTGATCTCTAGCCCTTGGGGCTTTGGGGC 390
   |||||
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrLeuThySerSerTyrValGlyAlaSerIle 40
   |||||
Db 391 ACACGTGGTTCACATGCTGCTCCCACTGGGAAACAAAGTTCTTATGTCGGTCCAGCATT 450
   |||||
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThrGly 60
   |||||
Db 451 GTGACAGCAGATTGGCTTCTCCAGGGCCTCTGATGGAATGGCCACACACAGCAGGC 510
   |||||
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
   |||||
Db 511 ATACCCAGGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 570
   |||||
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
   |||||
Db 571 CAGGCCATGATGGTGCATCATCAGTGCATCTCTCCCTGGCCCTGCATTATCTCTGTG 630
   |||||
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIlysaPaArgValAlaVal 119
   |||||
Db 631 GGCATGAGATGACAGACTTCTCTCCAGGAATCCGAGCAACAGAGTGGCGGTT 687
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```

RESULT 13

CA389170

LOCUS CA389170 459 bp mRNA linear EST 06-NOV-2002

DEFINITION cs06d06.y1 Human Retinal pigment epithelium/choroid cDNA

(Un-normalized, unamplified): cs Homo sapiens cDNA clone cs06d06

5', mRNA sequence.

ACCESSION CA389170

VERSION CA389170.1 GI:24719072

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 459)

Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,

Touchman,J.W., Bouffard,G., Smith,D., and Peterson,K.

Expressed sequence tag analysis of human RPE/choroid for the

NEIBank Project: Over 6000 non-redundant transcripts, novel genes

and splice variants

Mol. Vis. 8 (4), 205-220 (2002)

JOURNAL MEDLINE

PUBMED 22103460

COMMENT 12107410

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: Graeme@helix.nih.gov

Plate: 06 row: d column: 06

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

1. 459

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="cs06d06"

/tissue_type="RPE/choroid"

/dev_stage="Adult"

/lab_host="EMDH10B"

/clone_lib="Human Retinal pigment epithelium/choroid cDNA

(Un-normalized, unamplified): cs"

/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor

eyes (75-80 years old) yielded approximately 600 mg of

dissected RPE/choroid tissue. This in turn yielded 340 ug

of total RNA and 7 ug of mRNA. A directionally cloned cDNA

library in the pCMVSPORT6 vector was constructed at Life

Technologies (Rockville, MD; now part of Invitrogen Corp),

essentially following the protocols of the SuperScript

plasmid System (Invitrogen Corp

<http://www.invitrogen.com/>). The library code

designation was cs. For this library, cDNA inserts were

cloned into the NotI/Mui sites of the vector. EST

analysis was performed on the unamplified library at the

NIH Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:

Pred. No.:	6,556-100	Length:	459
Score:	113.00	Matches:	113
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	49.13%	Indels:	0
DB:	6	Gaps:	0

US-09-787-677A-3 (1-230) x CA389170 (1-459)

```

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTlleLeuGlyLeuLeuGlyLeuLeuGly 20
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Db 121 ATGGCCCTCTTGGCCCTCCCACTGGGCTGATCTCTAGCCCTTGGGGCTTTGGGGC 180
   |||||
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrLeuThySerSerTyrValGlyAlaSerIle 40
   |||||
Db 181 ACACGTGGTTCACATGCTGCTCCCACTGGGAAACAAAGTTCTTATGTCGGTCCAGCATT 240
   |||||
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThrGly 60
   |||||
Db 241 GTGACAGCAGATTGGCTTCTCCAGGGCCTCTGATGGAATGGCCACACACAGCAGGC 300
   |||||
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
   |||||
Db 301 ATACCCAGGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 360
   |||||
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
   |||||
Db 361 CAGGCCATGATGGTGCATCATCAGTGCATCTCTCCCTGGCCCTGCATTATCTCTGTG 420
   |||||
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAla 113
   |||||
Db 421 GGCATGAGATGACAGACTTCTCTCCAGGAATCCGAGCAACAGAGTGGCGGTT 459
   |||||

```

RESULT 14

CR554772

LOCUS CR554772 421 bp mRNA linear EST 12-JUL-2004

DEFINITION DKFZP469E0814.r1.469 (synonym: pki1) Pongo pygmaeus cDNA clone

(Un-normalized, unamplified): 5', mRNA sequence.

ACCESSION CR554772

VERSION CR554772.1 GI:50244701

KEYWORDS EST.

SOURCE Pongo pygmaeus (orangutan)

ORGANISM Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.

1 (bases 1 to 421)

Bloeker,H., Boecker,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C.,

Osanger,A., Fobo,G., Han,M., and Wiemann,S.

Pongo pygmaeus mRNA (Bloeker,H., Boecker,M., Brandt,P., et al.)

Unpublished (2004)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ),
Email: s.wiemann@dkfz-heidelberg.de, sequenced by GBF (National
Research Centre for Biotechnology Ltd., Braunschweig/Germany)
within the CDNA sequencing consortium of the German Genome Project.
This clone (DKFZP469E0814) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://mlps.gsf.de/projects/cdna/>.

FEATURES
source

1. 421
Location/Qualifiers
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP469E0814"
/issue_type="Kidney"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="469 (synonym: pKid1)"
/note="Vector: pSPORT1_Sfi; Site_1: SfiIA; Site_2: SfiIB"

ORIGIN

Alignment Scores:

	5.4e-98	Length:	421
Pred. No.:	111.00	Matches:	111
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	48.26%	Gaps:	0

US-09-787-677a-3 (1-230) x CRS54772 (1-421)

QY 1 MetAlaSerLeuGlyLeuGlnValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB 89 ATGGCCCTCTTGGCTTCAACCTGTGGGCTACATCCAGCCCTTCTGGGCTTTGGGC 148
QY 21 ThrIleuValMetIleuLeuProSerTrpIleuSerSerTrpValGlyAlaSerIle 40
DB 149 ACACTGGTGGCAGTGGCTCCCAAGCTGAAACAGATTCTTACGTGGTGGCCAGCAT 208
QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTrpMetGlyCysAlaTrpHisSerThrGly 60
DB 209 GTGACACAGTGGCTTCCAGAGGCTCTCGATGAGTGTGCACACACAGACAGGT 268
QY 61 IleThrGlnCysAapIleTyrSerThrIleuGlyLeuProAlaAapIleGlnAlaAla 80
DB 269 ATCACCAAGTGTGACATCTATAGCACCTTCTGGGCTGCGCGCTGACATCCAGGCTGCC 328
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 329 CAGGCCATGAGTGGACATCCAGTGCATCTCTCCGCGCTGCATTAATCTGTGGTG 388
QY 101 GlyMetArgCysThrValPheCysGlnGluSer 111
DB 389 GGCATGAGATGCACAGTCTTCTGCCAGGAATCC 421

RESULT 15
AI953481/c 560 bp mRNA linear EST 08-MAR-2000
LOCUS AI953481.1 GI:5745791
DEFINITION similar to TR:088552 088552 CLAUDIN-2.1, mRNA sequence.
ACCESSION AI953481
VERSION AI953481.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 560)
AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-rc@mail.nih.gov
Issue Procurement: Christopher Moskajuk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.lnl.gov/bdip/image/image.html
Insert Length: 756 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 430.

FEATURES
source

1. 560
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2472651"
/lab_host="DH108"
/clone_lib="NCI CGAP_Kid1"
/note="Organ: Kidney; Vector: pTRT3D-Pac (pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and as circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1322376-1323911, 1456007-1456755, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

ORIGIN

Alignment Scores:

	6.86e-97	Length:	560
Pred. No.:	110.00	Matches:	123
Score:	99.19%	Conservative:	0
Percent Similarity:	99.19%	Mismatches:	1
Best Local Similarity:	47.83%	Indels:	0
Query Match:	1	Gaps:	0

US-09-787-677a-3 (1-230) x AI953481 (1-560)

QY 29 SerTrpIleThrSerSerTrpValGlyAlaSerIleValThrAlaValGlyPheSerIys 48
DB 560 AGCTGAAACAGATTCTTATGTCGGTGCAGCATTTGTACAGCATTTGCTTCCAG 501
QY 49 GlyLeuTrpMetGlyCysAlaTrpHisSerThrGlyIleThrGlnCysAapIleTyrSer 68
DB 500 GGCTCTGATGAGATGTGCACACACACAGCATTCACCAAGTGTGACATTAAGC 441
QY 69 ThrIleuGlyLeuProAlaAapIleGlnAlaAlaGlnAlaMetMetValThrSerSer 88
DB 440 ACCCTTGTGGAGCTGCCCGCTGACATCCAGGCTGCCAGGSCATGAGTGCATCCAGT 381
QY 89 AlaIleSerSerLeuAlaCysIleIleSerValValGlyMetArgCysThrValPheCys 108
DB 380 GCATCTCTCCCTCGGCTGCATTAATCTGTGGTGGCAATGAGACAGATCTTTTGC 321
QY 109 GlnGluSerArgAlaValAapArgValAlaValAlaGlyValPhePheIleLeuGly 128
DB 320 CAGGAATCCGAGACCAAGACAGAGTGGCGGTACAGAGTGGAGCTTTTCACTCTTGA 261
QY 129 GlyLeuLeuGly-PheIleProValAlaTrpAsnLeuHisGlyIleLeuArgAapPheTyr 148
DB 260 GGCTCTTGGATTTATTCCTGTGGCTGGAAATCTTCATGGAGATCTTAAGGACTTTTA 201
QY 148 rSerProLeu 151
DB 200 CTCACCACTG 191

Search completed: December 20, 2004, 20:21:17
Job time : 3203 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 13:33:26 ; Search time 4299 Seconds

(without alignments)

2530.037 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 1174

Sequence: 1 MASLGQVGVYIGLGLG.....PGQPKVKSEFNSYSLTGYV 230

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US09787677/rnatc.20122004.132739.19435/app.query.fasta_1.391
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAFSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09787677_QCGN_1.1.3731 @rnatc.20122004.132739.19435 -NCPV=6 -ICPV=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_ste:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	693	6	CQ732222 Sequence
2	1174	100.0	693	9	AF250558 Homo sapi
3	1174	100.0	1400	6	AR340765 Sequence
4	1174	100.0	1400	6	BD085944 Elongatio

5	1174	100.0	1475	6	AX092348 Sequence
6	1174	100.0	1475	6	AX298996 Sequence
7	1174	100.0	1475	6	AX395213 Sequence
8	1174	100.0	1475	6	AX454606 Sequence
9	1174	100.0	1475	6	AX464358 Sequence
10	1174	100.0	1475	6	AX491084 Sequence
11	1174	100.0	1475	6	AX697065 Sequence
12	1174	100.0	1475	6	AX358474 Homo sapi
13	1174	100.0	1506	9	BC014424 Homo sapi
14	1174	100.0	1618	9	BC071747 Homo sapi
15	1174	100.0	1918	9	AF177340 Homo sapi
16	1174	100.0	2742	6	BD237562 Membrane-
17	1174	100.0	2863	6	AX136129 Sequence
18	1174	100.0	2863	6	BD123517 Secretory
19	1174	100.0	2863	9	AK075371 Homo sapi
20	1174	100.0	2959	9	AK075405 Homo sapi
21	1174	100.0	109465	9	AL158821 Human DNA
22	1170	99.7	1441	6	AX286822 Sequence
23	1162	99.0	693	6	AX497200 Sequence
24	1162	99.0	1524	6	AR340718 Sequence
25	1162	99.0	1524	6	BD085897 Elongatio
26	1119	95.3	953	4	AF358907 Canis fam
27	1114	94.9	1032	4	AB115779 Bos tauru
28	1099	93.6	239385	2	AC109686 Rattus no
29	1099	93.6	250600	2	AC136646 Rattus no
30	1099	93.6	268828	2	AC091513 Rattus no
31	1096	93.4	779	6	AX286824 Sequence
32	1096	93.4	791	6	B31591 E31591 Tight junct
33	1096	93.4	791	10	AF072128 Mus muscu
34	1096	93.4	2838	10	BC015252 Mus muscu
35	1096	93.4	184872	10	AL672243 BX934932 Gallus ga
36	792.5	67.5	1492	5	AX136475 Sequence
37	581	49.5	615	6	BD123715 Secretory
38	581	49.5	615	6	CQ734026 Sequence
39	571	48.6	720	6	AX133445 Homo sapi
40	571	48.6	720	9	HSAL32445 AX376286 Sequence
41	571	48.6	1174	6	AX468678 Sequence
42	571	48.6	1174	6	AX697255 Sequence
43	571	48.6	1174	6	AX358533 Homo sapi
44	571	48.6	1174	9	AY355349 Homo sapi
45	571	48.6	1227	9	AY355349 Homo sapi

ALIGNMENTS

RESULT 1
CQ732222
LOCUS CQ732222 693 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 18156 from Patent WO02068579.
ACCESSION CQ732222
VERSION CQ732222.1 GI:42311107
KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.

Kits, such as nucleic acid arrays, comprising a majority of

humanexons or transcripts, for detecting expression and other uses

thereof Patent: WO 02068579-A 18156 06-SEP-2002;

PE Corporation (NY) (US)

Location/Qualifiers

1. 693 /organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

FEATURES

source

ORIGIN

Alignment Scores: 9.53e-107 Length: 693
Pred. No.: 1174.00 Matches: 230
Score:

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-787-677A-3 (1-230) x CQ732222 (1-693)

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 DB 1 ATGGCCCTCTTGGCCCTTGCACATCTGAGGCTTCCAGGCTTCTGGGGCTTTTGGGC 60
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysSerSerTyrValAlaSerIle 40
 DB 61 ACACGTGTTCCAGTCGCTGCCAGCTGAGAAACAAGTTCTTATGCGGTGCAGCAT 120
 QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThyGly 60
 DB 121 GTGACAGCAGTTGGCTTCTCCAGGCGCTCGATGGAATGTGCCACACACAGCAGGC 180
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 DB 181 ATCAACCAGGTGACATCTATAGCACCCTTCTGGGCTGCCGCTGACATCCAGGCTGCC 240
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValIle 100
 DB 241 CAGGCCATGATGTGACATCCAGTCAGATCTCTCCCTGGGCTGCATTATCTCTGTG 300
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaAla 120
 DB 301 GGCGTGAATGACAGCTCTTCTCCAGGAATCCGACAGAAACAGAGTGGCGGTAGCA 360
 QY 121 GlyIleValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleTrpAsnLeu 140
 DB 361 GGTGAGTCTTTTTCATCTTGGAGGCTCTCGGAACTTCTCTGTTGCTGGAACTT 420
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 DB 421 CATGGATCTCAGGAGCTTCTACTACACACTGGTGCCTGACACAGAAATTTGAGATT 480
 QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 DB 481 GGAGAGCTCTTTTACTTGGGCAATATTTCTCCCTGTTCTCCGTATGAGTGCAGATCATC 540
 QY 181 LeuCyPheSerCysSerSerGlnArgAspArgSerAntTyrTyrAspAlaTyrGlnAla 200
 DB 541 CTCGCTTTTCTGCTCATCCAGAAATGCTCCAACTAGTACGATGCTTACCAAGCC 600
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
 DB 601 CAACCTTTGGCACAAGAGCTCTCCAAAGCTGTGTAACCTCCCAAAAGTCAAGAGTGA 660
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 661 TTCAATTCCTACACCTGACAGGATATGTG 690

RESULT 2

AF250558 693 bp mRNA linear PRI 10-JUN-2002
 LOCUS Homo sapiens claudin-2 mRNA, complete cds.
 DEFINITION AF250558
 ACCESSION AF250558
 VERSION AF250558.1 GI:9755008
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 693)
 Sakaguchi,T., Gu,X., Golden,H.M., Suh,E., Rhoads,D.B. and
 Reinecker,H.C.

REFERENCE
 AUTHORS
 TITLE
 Cloning of the human claudin-2 5'-flanking region revealed a
 TATA-less promoter with conserved binding sites in mouse and human
 for caudal-related homeodomain proteins and hepatocyte nuclear
 factor-1alpha

JOURNAL J. Biol. Chem. 277 (24), 21361-21370 (2002)
 MEDLINE 22050612
 PUBMED 11934881
 REFERENCE 2 (bases 1 to 693)
 AUTHORS Reinecker,H.-C., Sakaguchi,T. and Golden,H.M.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAR-2000) Gastrointestinal Unit, Massachusetts
 General Hospital, Fruit Street, Boston, MA 02114, USA
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ORIGIN

Alignment Scores:

Pred. No.: 9,53e-107 Length: 693
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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US-09-787-677A-3 (1-230) x AF250558 (1-693)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
 DB 1 ATGGCCCTCTTGGCCCTTGCACATCTGAGGCTTCCAGGCTTCTGGGGCTTTTGGGC 60
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysSerSerTyrValAlaSerIle 40
 DB 61 ACACGTGTTCCAGTCGCTGCCAGCTGAGAAACAAGTTCTTATGCGGTGCAGCAT 120
 QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThyGly 60
 DB 121 GTGACAGCAGTTGGCTTCTCCAGGCGCTCGATGGAATGTGCCACACACAGCAGGC 180
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 DB 181 ATCAACCAGGTGACATCTATAGCACCCTTCTGGGCTGCCGCTGACATCCAGGCTGCC 240
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValIle 100
 DB 241 CAGGCCATGATGTGACATCCAGTCAGATCTCTCCCTGGGCTGCATTATCTCTGTG 300
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaAla 120
 DB 301 GGCGTGAATGACAGCTCTTCTCCAGGAATCCGACAGAAACAGAGTGGCGGTAGCA 360
 QY 121 GlyIleValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleTrpAsnLeu 140
 DB 361 GGTGAGTCTTTTTCATCTTGGAGGCTCTCGGAACTTCTCTGTTGCTGGAACTT 420
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 DB 421 CATGGATCTCAGGAGCTTCTACTACACACTGGTGCCTGACACAGAAATTTGAGATT 480
 QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180

Db 481 GGAGAGCTTTTACTTGGGCTATTTCCTCCCTGCTCCGATGACGAAATATC 540
Qy 181 LeuCyBpSerCySerSerGlnArgAsnArgSerAntyTyTyRaPaLaTyGlna 200
Db 541 CTCGCTTTTCCGCTCATCCAGAGAAATCGCTCCAACTACTAGATGCTTACCAAGCC 600
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValysSerGlu 220
Db 601 CAACCTCTTCCCAAGAGAGCTCTCCAAAGGCTGTGTAACCTCCCAAGTCMAAGAGTAG 660
Qy 221 PheAsnSerTySerLeuThrGlyTyVal 230
Db 661 TTCAATTCTTACAGCTGACAGGATATGT 690
RESULT 3
AR340765 1400 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 139 from patent US 6573068.
DEFINITION AR340765
ACCESSION AR340765
VERSION AR340765.1 GI:33732507
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1400)
AUTHORS Mlne Edwards,V.-B.D., Ducleert,A. and Bougueleret,L.
TITLE Claudin-50 protein
JOURNAL Patent: US 6573068-A 139 03-JUN-2003;
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source location/Qualifiers
1..1400
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/mol_type="genomic DNA"
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Alignment Scores:
Pred. No.: 2,24e-106 Length: 1400
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyTrilleLeuGlyLeuLeuGlyLeuLeuGly 20
Db 36 ATGGCCCTCTTGGCCCTCAACCTGTGGGCTACATCTTAGGCCCTTGGGGCTTTTGGGC 95
Qy 21 ThrLeuValAlaMetLeuLeuProSerTrTyTrSerSerTyTyValGlyAlaSerIle 40
Db 96 ACACGTGTTCCATGCTGCTCCCAAGTGAACAAAGTTCTTATGCGGTGCGACGATC 155
Qy 41 ValThrAlaValGlyPheSerIysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 156 GTACACGACATTTGGCTTCTCCAAAGGCTCTGATGGAATGTGCCACACAGCAGGCG 215
Qy 61 IleThrGlnCysAspIleTySerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 216 ATCACCAGTGTGACATCTATAGCACCTTCTGGGCTGCCCGCTGACATCCAGGCTGCC 275
Qy 81 GlnAlaMetMetValThrSerSerAlaHisSerSerLeuAlaCysIleIleSerVal 100
Db 276 CAGGCCATGTATGTGATCATCAGTCAATCTCCCTCGCTGCTGACATATCTGTGTG 335
Qy 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
Db 336 GGCATGAGATGCACAGCTTCTGCCAGAAATCCGAGACCAAGACAGAGTGGCGTAGCA 395
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
Db 396 GGTGGAGTCTTTTTCATCTTTGAGGCGCTCTGGGATTCATCTCTGTGCTGGAATCTT 455

Qy 141 HieGlyIleLeuArgAspPheTySerSerProLeuValProAspSerMetLysPheGlnIle 160
Db 456 CATGGATCTTACGGAGCTTCTACTCACCTGTGCTTACAGCATGAATTTGAATTT 515
Qy 161 GlyGlnAlaLeuTyTrilleLeuSerSerLeuPheSerLeuIleAlaGlyIle 180
Db 516 GGAGAGCTTTTACTTGGGCTATTTCCTCCCTGCTCCGATAGCTGAAATATC 575
Qy 181 LeuCyBpSerCySerSerGlnArgAsnArgSerAntyTyTyRaPaLaTyGlna 200
Db 576 CTCGCTTTTCCGCTCATCCAGAGAAATCGCTCCAACTACTAGATGCTTACCAAGCC 635
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValysSerGlu 220
Db 636 CAACCTCTTCCCAAGAGAGCTCTCCAAAGGCTGTGTAACCTCCCAAGTCMAAGAGTAG 695
Qy 221 PheAsnSerTySerLeuThrGlyTyVal 230
Db 696 TTCAATTCTTACAGCTGACAGGATATGT 725
RESULT 4
BD085944 1400 bp DNA linear PAT 27-AUG-2002
LOCUS Elongation CDNA of secretory protein.
DEFINITION BD085944
ACCESSION BD085944
VERSION BD085944.1 GI:22631554
KEYWORDS JP 2001523453-A/86.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1400)
AUTHORS Bougueleret,L., Ducleert,A. and Edwards,J.B.D.M.
TITLE Elongation CDNA of secretory protein
JOURNAL Patent: JP 2001523453-A 86 27-NOV-2001;
GENSET
OS Homo sapiens (human)
PN JP 2001523453-A/86
PD 27-NOV-2001
PR 13-NOV-1998 JP 2000521191
PR 13-NOV-1998 US 60/066677,17-DEC-1997 US 60/069957 PR
09-FEB-1998 US 60/074121,13-APR-1998 US 60/081563 PR
10-AUG-1998 US 60/096116,04-SEP-1998 US 60/099273 PR LYDIE
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C12N1/21,
PC C12N5/10,C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC
Von Heijne matrix
CC score 5.6399980926514
seq IIGLGLGLTLVA/KL
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Alignment Scores:
Pred. No.: 2,24e-106 Length: 1400
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyTrilleLeuGlyLeuLeuGlyLeuLeuGly 20

Db 36 ATGGCCCTCTTGAGCCTCAACTGTGGGGCTACATCCAGGCTTCTGAGGCTTTTGAGGC 95
 Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpLyThrSerSerLyValAlaSerIle 40
 Db 96 ACCTGGTTCGCAATGCTGCTCCCGAGCTGGMAAACAAGTTCTTATGTCGGGCGACGATT 155
 Qy 41 ValThrAlaValAlaGlyPheSerLyGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
 Db 156 GTGACACAGATTGGCTTCTCCAGAGGCTCTGGATGGAAATGGCCACACACAGCAGAGGC 215
 Qy 61 IleThrGlnCysAspIleTySerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 Db 216 ATACCCAGAGTGATCATCTATAGCACCTTCTGGGCTGCGCGTGACATCCAGGCTGCC 275
 Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 276 CAGGCCATGATGGAGATCCAGATCCATCTCCCTGGGCTGCAATTAATCTGTGGTG 335
 Qy 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaLysAspArgValAlaValAla 120
 Db 336 GGCATGAGATGACAGCTTCTGCGCAGAAATCCGAGCCAAAGACAGATGGCGGTAGCA 395
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 Qy 141 HisGlyIleLeuAlaGlyPheTySerProLeuValProAspSerMetLysPheGlnIle 160
 Db 456 CATGGAGTCTTCACGGGACTTCTACTACACATGGTGCTGACAGCAATGAATTTGAAATT 515
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 Db 576 CTCTGCTTTTCTCTCATCCAGAAATCGCTCCAACTACTAGATGCTTACCAAGCC 635
 Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
 Db 636 CAACCTTTCGCAAGAGAGCTCTCCAAAGGCTGTCAACCTCCCAAGTCMAAGAGTGAG 695
 Qy 221 PheAsnSerTySerLeuThrGlyTyVal 230
 Db 696 TTCAATTCCTACAGCTGACAGGATATGTG 725
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 LOCUS AX092348 1475 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 79 from Patent WO0116318.
 ACCESSION AX092348
 VERSION AX092348.1 GI:13444488
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
 Wood,W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0116318-A 79 08-MAR-2001;
 Genentech, Inc. (US)
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
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Pred. No.: 2,38e-106 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
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 Db 182 ACCTGGTTCGCAATGCTGCTCCCGAGCTGGMAAACAAGTTCTTATGTCGGGCGACGATT 241
 Qy 41 ValThrAlaValAlaGlyPheSerLyGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
 Db 242 GTGACACAGATTGGCTTCTCCAGAGGCTCTGGATGGAAATGGCCACACACAGCAGAGGC 301
 Qy 61 IleThrGlnCysAspIleTySerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 Db 302 ATACCCAGAGTGATCATCTATAGCACCTTCTGGGCTGCGCGTGACATCCAGGCTGCC 361
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 Db 362 CAGGCCATGATGGAGATCCAGATCCATCTCCCTGGGCTGCAATTAATCTGTGGTG 421
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 Db 422 GGTGAGATGATGACAGCTTCTGCGCAGAAATCCGAGCCAAAGACAGATGGCGGTAGCA 481
 Qy 121 GlyIleValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
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 Db 602 GAGAGGCTCTTTACTGCGGCTTATTTCTTCTCTGTCCTGATAGCTGGAAATCATC 661
 Qy 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAntyTyTyAspAlaTyGlnAla 200
 Db 662 CTCTGCTTTTCTCTCATCCAGAAATCGCTCCAACTACTAGATGCTTACCAAGCC 721
 Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
 Db 722 CAACCTTTCGCAAGAGAGCTCTCCAAAGGCTGTCAACCTCCCAAGTCMAAGAGTGAG 781
 Qy 221 PheAsnSerTySerLeuThrGlyTyVal 230
 Db 782 TTCAATTCCTACAGCTGACAGGATATGTG 811
 RESULT 6
 LOCUS AX299996 1475 bp DNA linear PAT 26-NOV-2001
 DEFINITION Sequence 1 from Patent WO0166740.
 ACCESSION AX299996
 VERSION AX299996.1 GI:17129473
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Eaton,D.L., Fong,S., Goddard,A., Godowski,P.J., Grimaldi,C.J.,
 Gurney,A.L., Tumas,D., Watanabe,C.K., Wood,W.I. and Zhang,Z.
 TITLE Compositions and methods for the treatment of immune related
 diseases

JOURNAL		Patent: WO 0166740-A 1 13-SEP-2001;	
Genentech, Inc. (US)			
FEATURES	Location/Qualifiers		
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Pred. No.:	2,38e-106	Length:	1475
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
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QY	1	MetaLaseLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly	20
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QY	21	ThirLeuValAlaMetLeuLeuProSerTrrPlyThrSerSerTyrValGlyAlaSerIle	40
Db	182	ACACTGTGTGCATGCTGCTCCCAAGCTGGAAAAAAGTTCTTAGTGTGGTCCAGCATT	241
QY	41	ValThrAlaValGlyPheSerIleGlyLeuTrrMetGluCysAlaThrHisSerThrGly	60
Db	242	GTGACAGAGATTGGCTTCTCCAAAGGGCTCTGGATGGATGGATGCCACACAGCAGCC	301
QY	61	IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla	80
Db	302	ATCACCCAGTGTGACATCTATAGCACCCTTCTGGGCTGCGCTGACATCCAGGCTGCC	361
QY	81	GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysAlleIleSerValVal	100
Db	362	CAGGCCATGATGGTGACATCCAGTGCATCTCTCTGGCTGCTGCAATTATCTCTGGGTG	421
QY	101	GlyMetArgCysThrValPheCysGlnGlnSerArgAlaAlaCysAspArgValAlaValAla	120
Db	422	GGCATGAGATGCACAGCTTCTTCCGACGAATCCGAGCAAAAGACAGGTGGCGTTAGCA	481
QY	121	GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu	140
Db	482	GGTGGAGCTTTTTCATCTTGGAGGCTCTCGGATTCATTCTCGTGGCTGGAATCTT	541
QY	141	HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle	160
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Db	602	GGAAGAGCTCTTACTTGGGCATTTATTTCTTCCCTGTTCTCCCTGATAGCTGAATCATC	661
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Db	722	CAACCTCTTGGCACAAAGAGCTTCTCAAGGCTGTGCTCAACTCCCAAGTCAAGAGTAG	781
QY	221	PheAsnSerTyrSerLeuThrGlyTyrVal	230
Db	782	TTCAATTCTTACAGCTGACAGGGATGTG	811
RESULT 7			
LOCUS	AX395213	1475 bp	DNA
DEFINITION	Sequence 1 from Patent WO0216429.		linear
ACCESSION	AX395213		PAT 18-MAY-2002
VERSION	AX395213.1	GI:21066244	

KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
AUTHORS	Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Potakis, P., Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.				
TITLE	Compositions and methods for the diagnosis and treatment of tumor Patent: WO 0216429-A I 28-FEB-2002;				
JOURNAL	Genentech, Inc. (US)				
FEATURES	Location/Qualifiers				
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ORIGIN	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"				
Alignment Scores:					
Pred. No.:	2,38e-106	Length:	1475		
Score:	1174..00	Matches:	230		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	6	Gaps:	0		
US-09-787-677A-3 (1-230) x AX395213 (1-1475)					
QY	1 MetAlSerIenGlyLeuEnlInleuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly	20			
Db	122 ATGGCTCTCTTGCGCTCCAACTTGTGGCTACATCCTTAAGGCCTTTGGGCTTTGGGC	18			
QY	21 ThrLeuValAlaMetLeuLeuProSerTrpIySThrSerSerTyValGlyAlaSerIle	40			
Db	182 ACAGTGGTTCATGTGTGCTCCCAAGCTGAAGAAAACAATTCTTAGTGTGGCCAGCAT	24			
QY	41 ValThAlaValGlyPheSerIySeGlyLeuTrpMetGluCyValArThHisSerThrGly	60			
Db	242 GTGACAGCAGTGGCTTCTCCAAAGGCCCTGTGGATGTGCACACAGCACAGCAGGC	30			
QY	61 IleThrGlyCyAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla	80			
Db	302 ATCAACCAGTGTGACATCTTAGACACCCCTTCTGGGCTGGCCGCTGACATCAGGCTGC	36			
QY	81 GlnAlaMetValThrSerSerAlaIleSerSerLeuAlaCySileIleSerValVal	100			
Db	362 CAGGCATGATGGTGTGACATCCAGTCGATCTCTCCGCGCTGATTAATCTGTGGTG	42			
QY	101 GlyMetArgCySerThyValPheCysGlnGlnSerArgAlaValSAAPArgValAlaValAla	120			
Db	422 GGCATGATGACACAGTCTTCTGCCAGGAATCCGAGCAAAGAAGAGTGGCGTGACA	48			
QY	121 GlyGlyValPhePheIleLeuGlyValLeuLeuGlyPheIleProValAlaTrpAsnLeu	140			
Db	482 GGtGGAGCTTTTTCACTCTGGAGGCCCTCCGGGATTCATTCCTGTGGCTGGAATCTT	54			
QY	141 HisGlyIleLeuArgAspPheTySerProLeuValProAspSerMetIyPheGlnIle	160			
Db	542 CATGGATCTTACGGGACTTCTACTACACACAGTGGTGTGACAGATGAATTTGAGATT	60			
QY	161 GlyGlyAlaLeuTyRleuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle	180			
Db	602 GGAGAGGCTCTTAACTTGGGCAATTAATTTCTTCCCTGCTTCCCTGATGATGGAATCATC	66			
QY	181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTrpIyTrpAspAlaTyGlnAla	200			
Db	662 CTCGTGTTTCTTCGCTCATCCCAAGGAATGGCTCCAATACTACATCGATGCGCTTACCAAGCC	72			
QY	201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValIySerGlu	220			
Db	722 CAACCTCTTGGCCACAGAGACTCTTCAAGGCGCTGTGATCACTCCCAAGATCAAGAGTAG	78			
QY	221 PheAsnSerTyRserLeuThrGlyTyVal	230			

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Db      782 TTCAATTCTTACAGCCTGACAGGATATGTG 811
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RESULT 8
LOCUS   AX454606 1475 bp DNA linear PAT 06-JUL-2002
DEFINITION
Sequence 191 from Patent WO0208284.
ACCESSION AX454606
VERSION  AX454606.1 GI:21713927
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurey,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.P., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0208284-A 191 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
FEATURES
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ORIGIN
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Pred. No.:      2,38e-106      Length:      1475
Score:          1174.00      Matches:      230
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             Gaps:        0
US-09-787-677a-3 (1-230) x AX454606 (1-1475)
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Db      122 ATGGCCCTCTTGCCCTTCAACCTGTGGGCTACATCTCAGCCTTCTGGGGCTTTGGGC 181
QY      21 ThrIleuValAlaMetLeuLeuProSerTrpIyThrSerSerTrpValGlyAlaSerIle 40
Db      182 ACCTGGTTCGCAAGCTGCTCCAGCTGAAAAACAAGTTCTTGTGCGGGCCAGCATT 241
QY      41 ValThrAlaValGlyPheSerTrpGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db      242 GTGACACAGATTGGCTTCTCCAGAGGCTCTGAGATGGAATGTCACACACACAGCAGGC 301
QY      61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db      302 ATCACCAGTGTGACATCTATAGCACCTTCTGGGCTGCGCGCTGACATCCAGGCTGCC 361
QY      81 GlnAlaMetLeuValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db      362 CAGGCCATGATGAGATCCAGTCAATCTCCCTCGGCTCATTAATCTCTGTGGTG 421
QY      101 GlyMetArgCysTrpValPheCysGlnGluSerArgAlaIleAspArgValAlaValAla 120
Db      422 GGCATGATGATCAACATCTTCTGCCAGAAATCCGAGCCAAAGACAGATGGCCGTACA 481
QY      121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
Db      482 GGTGAGATCTTTTCATCTTGAAGGCTCTGGGATTCATTCGTGGCTGGAACTTT 541

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QY      141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db      542 CATGGATCTTACAGGACCTTCTACTACACATGCTGCTGACAGCATGAATTTGAGATT 601
QY      161 GlyAlaLeuValTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db      602 GGAAGGCTCTTACTTGGGCAATTAATTTCTTCCCTGTCTCCGTAGTCGAAATCATC 661
QY      181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db      662 CTCTGCTTTTCCCTGCTCATCTCCAGAAAAATGCTCCAAATCTACATGATGCTTCAAGCC 721
QY      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValLysSerGlu 220
Db      722 CAACCTTTCGCCAAGAGACCTTCCAGGCTGTGTCACCTCCCAAGTCAGAGTGAG 781
QY      221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db      782 TTCAATTCTTACAGCCTGACAGGATATGTG 811
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RESULT 9
LOCUS   AX464358 1475 bp DNA linear PAT 16-JUL-2002
DEFINITION
Sequence 491 from Patent WO0140466.
ACCESSION AX464358
VERSION  AX464358.1 GI:21699195
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Baker,K.P., Beresini,M., DeForge,L., Desnoyers,L., Fljaroff,E.,
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Wood,W.L. and Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
same
Patent: WO 0140466-A 491 07-JUN-2001;
Genentech Inc. (US)
FEATURES
source      1..1475
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.:      2,38e-106      Length:      1475
Score:          1174.00      Matches:      230
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             Gaps:        0
US-09-787-677a-3 (1-230) x AX464358 (1-1475)
QY      1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
Db      122 ATGGCCCTCTTGCCCTTCAACCTGTGGGCTACATCTCAGCCTTCTGGGGCTTTGGGC 181
QY      21 ThrIleuValAlaMetLeuLeuProSerTrpIyThrSerSerTrpValGlyAlaSerIle 40
Db      182 ACATGGTTCGCAAGCTGCTCCAGCTGAAAAACAAGTTCTTGTGCGGGCCAGCATT 241
QY      41 ValThrAlaValGlyPheSerTrpGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db      242 GTGACACAGATTGGCTTCTCCAGAGGCTCTGAGATGGAATGTCACACACAGCAGGC 301
QY      61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db      302 ATCACCAGTGTGACATCTATAGCACCTTCTGGGCTGCGCGCTGACATCCAGGCTGCC 361

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QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCGCATGATGGATGACATCCAGTGCATCTCTCCCTGGCGCATTAATCTCTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIysAspArgValAlaValAla 120
DB 422 GGCATGATGACACAGCTCTTCTCCAGAGATCCGAGCCAAAGACAGATGGCGTGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIlePasnLeu 140
DB 482 GGTGAGATCTTTTCACTTCCTTGGAGGCGCTCTGGGATTCATTCCTGTGCTGGAACTT 541
QY 141 HisGlyTlleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CATGGATCTCTAGGGACCTTCTACTCAACACTGGTGCCTACAGCATGAATTTGAGATT 601
QY 161 GlyGlyAlaLeuValYrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 602 GAGAGGCTCTTACTTGGCATTAATTTCTCCCTGTCTCCCTGATAGCTGGAATCATC 661
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
DB 662 CTCTGCTTTTCCGTCTCATCCAGAGAAATCGCTCCAACTACTACATGCTTCAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 722 CAACCTCTTGCCCAAGAGAGCTCTCCAAAGCCGTGTCAACCTCCCAAGTCAAGAGTGA 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCATTTCTACAGCTGACAGGGTATGTG 811

RESULT 10
AX491084 1475 bp DNA linear PAT 16-AUG-2002
LOCUS Sequence 191 from Patent WO0200690.
DEFINITION AX491084
ACCESSION AX491084
VERSION AX491084.1 GI:22323879
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0200690-A 191 03-JAN-2002;

TITLE
JOURNAL
Genentech, Inc. (US)
Location/Qualifiers

FEATURES
source 1..1475
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 2,38e-106 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-787-677A-3 (1-230) x AX491084 (1-1475)

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DB 122 ATGGCTCTCTTGGCTCCAACTTGGGCTACATCTTAGGCTTCTGGGGCTTTTGGGC 181

QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValGlyAlaSerIle 40
DB 182 ACACGTGTGGCCATGTGTCTCCACAGTGAAGAAATTTTATGTGGTGGACAT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTyrMetGlyCysValAlaThrHisSerThrGly 60
DB 242 GTACAGCAGTGGCTTCTTCCAGAGGCTCTGTGATGAAATGTCCACACAGCACAGGCC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaIle 80
DB 302 ATCACCAGATGATCATCTATACACCTTCTGGGCTGCGCTGCATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCGCATGATGGATGACATCCAGTGCATCTCTCCCTGGCGCATTAATCTCTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIysAspArgValAlaValAla 120
DB 422 GGCATGATGACACAGCTCTTCTCCAGAGATCCGAGCCAAAGACAGATGGCGTGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIlePasnLeu 140
DB 482 GGTGAGATCTTTTCACTTCCTTGGAGGCGCTCTGGGATTCATTCCTGTGCTGGAACTT 541
QY 141 HisGlyTlleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CATGGATCTCTAGGGACCTTCTACTCAACACTGGTGCCTACAGCATGAATTTGAGATT 601
QY 161 GlyGlyAlaLeuValYrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 602 GAGAGGCTCTTACTTGGCATTAATTTCTCCCTGTCTCCCTGATAGCTGGAATCATC 661
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
DB 662 CTCTGCTTTTCCGTCTCATCCAGAGAAATCGCTCCAACTACTACATGCTTCAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 722 CAACCTCTTGCCCAAGAGAGCTCTCCAAAGCCGTGTCAACCTCCCAAGTCAAGAGTGA 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCATTTCTACAGCTGACAGGGTATGTG 811

RESULT 11
AX697065 1475 bp DNA linear PAT 02-APR-2003
LOCUS Sequence 133 from Patent WO0078961.
DEFINITION AX697065
ACCESSION AX697065
VERSION AX697065.1 GI:29498042
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
Eaton,D.L., Gao,W.O., Pan,J., Botstein,D., Fong,S., Goddard,A.,
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0078961-A 133 28-DEC-2000;

TITLE
JOURNAL
Genentech Inc. (US)
Location/Qualifiers

FEATURES
source 1..1475
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 2,38e-106 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-787-677A-3 (1-230) x AY358474 (1-1475)

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 DB 122 ATGGCCCTCTTGCCCTCCAACTGTGGGCTACATCTAGCCCTTCTGGGGCTTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysSerSerTyrValGlyAlaSerIle 40
 DB 182 ACACGTGTCCACAGCTGCTCCACAGTGAACCAAGTTTATGTCGGGCGACGACATT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGlyCysAlaTrpHisSerThrGly 60
 DB 242 GTGACAGCAGTGGCTTCTCCAAAGGCTCTGGATGGAATGTGCCACACACAGCAGCGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 DB 302 ATCACCCAGTGTGACATCTATAGCACCCCTCTGGGCTGCCCGCTGACATCCAGGCTGCC 361
 QY 81 GluAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 362 CAGGCCATGATGAGACATCCAGTCAATCTCCCTGGCTGCTCATTAATCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
 DB 422 GGCATGAGATGACAGCTTCTGTCAGGAATCCGACGCCAAGACAGATGGCGGTGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
 DB 482 GGTGAGTCTTTTCATCTGAGGCTCTCCGTGGAATTCATCTGTGCTGGAACTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 DB 542 CATGGATCTTCCAGGACTTCTACTCACTGATGCTGTCACACAGAAATTTGAAATT 601
 QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 DB 602 GAGAGGCTCTTATCTGGCATTAATTTCTTCTGTTCTCCGTAGACGCGAATCATC 661
 QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAntyTyrIleAspAlaTyrGlnAla 200
 DB 662 CTCTGCTTTCTGCTCATCCAGAGAAATGCTCCAACTACTACGATGCTTACCAAGCC 721
 QY 201 GluProLeuAlaTrpArgSerSerProArgProGlyGlnProPolysValIleSerGlu 220
 DB 722 CAACCTTGTGCACAAAGAGCTCTCCAAAGGCTGATCACTCCCAAGATCAAGAGTGA 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 782 TTCAATTCCTACACCTGACAGGATATGTG 811

RESULT 12
 AY358474 1475 bp mRNA linear PRI 03-OCT-2003
 LOCUS Homo sapiens clone DNA4886 Claudin-2 (UNQ705) mRNA, complete cds.
 DEFINITION AY358474
 ACCESSION AY358474
 VERSION AY358474.1 GI:37182070
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 1475)
 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.B.,
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,

Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
 Schoenfeld,J., Seashagiri,S., Simmons,L., Singh,J., Smith,Y.,
 Stinson,J., Vagstad,A., Vandlen,R., Watanabe,C., Wiand,D., Woods,K.,
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
 Goddard,A., Wood,W.I. and Godowski,P.
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment
 Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL
 PUBMED
 12975309
 2 (bases 1 to 1475)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Submitted (01-NOV-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA
 Location/Qualifiers

FEATURES
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 /mol_type="mRNA"
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 GFSGAMMECATSTGITOCDIYSTLLGIPADIOAAMVTSASLSLACISVVG
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 GEAHYGITISLSFLIAGTILLCFSCSQNRNSRYAYQAQPLATSSRPQGPAPVK
 SEPNYSYSLTGYV"

ORIGIN
 Alignment Scores:
 Pred. No.: 2,38e-106 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-787-677A-3 (1-230) x AY358474 (1-1475)

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 DB 122 ATGGCCCTCTTGCCCTCCAACTGTGGGCTACATCTAGCCCTTCTGGGGCTTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysSerSerTyrValGlyAlaSerIle 40
 DB 182 ACACGTGTCCACAGCTGCTCCACAGTGAACCAAGTTTATGTCGGGCGACGACATT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGlyCysAlaTrpHisSerThrGly 60
 DB 242 GTGACAGCAGTGGCTTCTCCAAAGGCTCTGGATGGAATGTGCCACACACAGCAGCGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 DB 302 ATCACCCAGTGTGACATCTATAGCACCCCTCTGGGCTGCCCGCTGACATCCAGGCTGCC 361
 QY 81 GluAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 362 CAGGCCATGATGAGACATCCAGTCAATCTCCCTGGCTGCTCATTAATCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
 DB 422 GGCATGAGATGACAGCTTCTGTCAGGAATCCGACGCCAAGACAGATGGCGGTGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140

Db 482 GGTGAGTCTTTTTCATCTTGAGAGGCTCTGGATTCTTCTGTGCTGGAACTT 541

Qy 141 HIGLIIYIleuArgaspPheTYrSerProleuValProaspSerNetlyspheGluIle 160

Db 542 CATGGATCTCAAGGAGCTTCTACTCAACCTGCTGCTCAAGCATGAATTTGAGATT 601

Qy 161 G1G1uAla1leuTYrleuGlyIleIleSerSerleuPheSerleuIleAlaGlyIleIle 180

Db 602 GAGAGGCTCTTACTTGGGCAATTATTCCTGTTCTCCCTGATGAGCTGAATCATC 661

Qy 181 LeuCySPheSerCySerSerGlnArgAsnArgSerAsnTYrTYrAspAlaTYrGlnAla 200

Db 662 CTCTGCTTTTCCGCTCATCTCCAGAGAAATGGCTCCAACTACTACATGCTTCCAGGCC 721

Qy 201 G1nProleuAlaThraArgSerSerProArgProGlyGlnProProlyValIlySerGlu 220

Db 722 CAACCTCTTGCCACAGAGAGCTCTCCAGAGCTGTGTCACCTCCCAAGTCACAGAGTAG 781

Qy 221 PheAsnSerTYrSerleuThraGlyTYrVal 230

Db 782 TTCAAATTCCTACAGCTGACAGGGTATGTG 811

RESULT 13

BC014424 1506 bp mRNA linear PRI 29-JUN-2004

LOCUS BC014424

DEFINITION Homo sapiens claudin 2, mRNA (cDNA clone MGC:20191 IMAGE:4645075), complete cds.

ACCESSION BC014424

VERSION BC014424.1 GI:15680158

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1506)

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klauener, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, A.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stappleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, L., Carninci, P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwen, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richardson, S., Wille, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schultz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1506)

Strausberg, R.

Direct Submission

Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomes Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs-rc@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

Info@cgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liso, Kim Macdonald, Amara Mason, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lisa Prabhu, Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalske, Duane Smalhus, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>

Series: IRAL Plate: 29 Row: m Column: 11

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9966780.

Location/Qualifiers

1. 1506

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="MGC:20191 IMAGE:4645075"

/issue_type="Colon, adenocarcinoma"

/clone_lib="NIH MGC 15"

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/note="Vector: pOTB7"

1. 1506

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/db_xref="LOCUSID:9075"

122. 814

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ORIGIN

Alignment Scores:

Pred. No.: 2,44e-106 Length: 1506

Score: 1174.00 Matches: 230

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-787-677A-3 (1-230) x BC014424 (1-1506)

Qy 1 Meta1SerleuGlyleuGlnleuValGlyTYrIleleuGlyleuGlyleuGly 20

Db 122 ATGGCTCTCTTGCTGCTCCAACTTGCGGCTCATCTGAGCTTCTGGGCTTTGGGC 181

Qy 21 ThrLeuValAlaMetleuLeuProSerTPlyrThrSerSerTYrValGlyAlaSerIle 40

Db 182 ACACGTGTTGCCATGTGCTGCCACAGTGAAGAAACAAGTTCTTATGTCGTCACACATT 241

Qy 41 ValThraAlaValGlyPheSerIlyleuTYrMetGluCysAlaThraIlySerThraGly 60

Db 242 GTACACAGAGTGGCTTCCCAAGGGCTCTGTGATGAATGTGCCACACACACAGAGGC 301

Qy 61 IleThraGlnCyAspIlyleTYrSerThraLeuGlyIleuProAlaAspIleGlnAla 80

Db 302 ATACCCAGTGTACATCTATAGCACCTTCTGGGCTGCCCTGACATCCAGGCTGCC 361

Qy 81 GlnAlaMetMetValThraSerSerAlaIleSerSerleuAlaCysIleIleSerVal 100

Db 362 CAGGCATATGATGTGACATCCAGTGAATCTCTCCCTGCGCATTTATCTCTGTGGTG 421

Qy 101 GlyMetArgCySerThraIlyPheCyGlnGlnuserArgAlaIlyAspArgValAlaVal 120

DB 422 GGCATGATGACAGACTCTTCTGCGCAGAAATCCGAGCAAGACAGAGTGGCGGTAGCA 481

QY 121 G1YGLYVALPHEPHELEULENGLYLEULENGLYPHELEULENGLYLEULENGLYLEULENGLY 140

DB 482 GGTGGAGCTCTTTCATCTTGAGAGGCTCTGAGATTCTCTGTTGCTTGGAATCTT 541

QY 141 H1AG1Y1LEULENGYAPHEPHELEULENGLYLEULENGLYLEULENGLYLEULENGLYLEULENGLY 160

DB 542 CATGGATCTTACGGAGCTTCTACTCCACTGCTGCTGACAGACATGAAATTTGAGATT 601

QY 161 G1YGLYVALPHEPHELEULENGLYLEULENGLYLEULENGLYLEULENGLYLEULENGLY 180

DB 602 GAGAGGCTCTTACTGAGCATATTTCTTCTGTTCTGCTGATGATGCTGAGATCATC 661

QY 181 LEUCYEPHESECYSESERSEGINATGASNAAGSERSENTYTYTAAPALATYTG1A1A 200

DB 662 CTCTGCTTTTCCGCTCATCCAGAGAAATCGCTCCCACTACATGATGCTTACCAAGCC 721

QY 201 G1NPROLEUALATFATGASERSEPRATGPRG1YGINPROLYVALYLYSSEGLU 220

DB 722 CAACCTTTTGCCACAGAGAGCTCTCCAGGCTGCTGACCTCCCAAGTCAAGAGTGTAG 781

QY 221 PHEANSEYTYRSELEULENGLYTYRVAL 230

DB 782 TTCATTCCTACAGCTGACAGGATATGTG 811

RESULT 14

BC071747

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

PUBMED

REFERENCE

TITLE

STRASBERG, R.

Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Falckovits

cDNA Library Preparation: CLOWTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www.shgc.stanford.edu>

Contact: (Dickson, Mark) md@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Series: IRAL Plate: 57 Row: n Column: 5

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9966780.

FEATURES

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/db_xref="taxon:9606"

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/clone_1lb="NIH MGC_186"

/lab_host="DH10B"

/note="Vector: pDNR-L1B"

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328..1020

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ORIGIN

Alignment Scores:

Pred. No.: 2,67e-106

Score: 1174.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 9

DB: 9

US-09-787-677A-3 (1-230) x BC071747 (1-1618)

QY 1 MetAlaSerLeuNGLYLENGLYLENGLYLENGLYLENGLYLENGLYLENGLYLENGLY 20

DB 328 ATGGCTCTTCTGCTCCCACTTGAGGCTGATCTCTAGCCCTTCTGAGCTTTGGGC 387

QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLeuThrSerSerTrpValAlaSerLe 40

DB 388 ACACGTGTCATGCTGCTCCAGCTGAGAAACAGTTCTTATGTCGATGACAGATT 447

QY 41 ValThrAlaValGlyPheSerLeuLeuTrpMetGluCysAlaThrHisSerThrGly 60

DB 448 GTGACAGACAGTGGCTTCTCCAGAGGCTCTGATGAGTGCACACACAGACAGGC 507

QY 61 IleThrGlnCysAspIleTrpSerThrLeuNGLYLENGLYLENGLYLENGLYLENGLY 80

DB 508 ATCACCCAGGTGACATCTTAGACACCTTCTGAGCTGCGCTGCATCCAGCTGCC 567

QY 81 G1NAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100

DB 568 CAGGCTATGATGATCATCATGATCATCTCTCTGCTGCTGATATCTCTGCTG 627

QY 101 G1YMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAla 120

Db 628 GGCATGATGATGACAGACTCTTCTCCAGAAATCCGAGCAAGAGAGAGTGGCGGTAGCA 687
Qy 121 GYGLYVAlPhehelIleuGLYleuLeuGLYPhelIleProValAlaTPaenLeu 140
Db 688 GGTGAGGCTTTTTCATCTTGGAGGCTCTGGGATTCATTCCTGTGGCTGGAACTT 747
Qy 141 HieGLYIleuArgaspPheTYrSerProLeuValProaspSerMetLysPheGluLe 160
Db 748 CATGGATCTTACGGAGCTTCTACTACCACTGGTGGCTTACAGCATGAATTTGAGATT 807
Qy 161 GYGLYAlaLeuTYrleuGLYIleIleSerSerLeuPheSerLeuIleAlaIle 180
Db 808 GAGAGGCTCTTACTTGGCATTTTCTTCCTGTTCCTCGATAGCTGGAATATC 867
Qy 181 LeuCyPheSerCySerSerGlnArgaspArgSerAsnTYrTraspAlaTYrGlnAla 200
Db 868 CTCTGCTTTTCCGCTCATCTCCAGAAATCGCTCCAACTACATACGATGCTTACCAAGCC 927
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
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Db 988 TTCAATTCTACAGCTGACAGGGTATGTG 1017

RESULT 15
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LOCUS Homo sapiens clone sp82 claudin 2 mRNA, complete cds.
DEFINITION AF177340
ACCESSION AF177340.1 GI:10503979
VERSION AF177340.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1918)
AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P.,
Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,
Yu,J. and Han,L.H.
TITLE Novel human cDNA clone with function of inhibiting cancer cell
growth
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1918)
AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P.,
Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,
Yu,J. and Han,L.H.
TITLE Direct Submission
JOURNAL Submitted (06-AUG-1999) National Laboratory For Oncogenes & Related
Genes, Shanghai Cancer Institute, 25/Ln 220 Xie Tu Road, Shanghai
200032, P.R. China
FEATURES
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ORIGIN
Alignment Scores: 3.28e-106 Length: 1918
Pred. No.:

Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-787-677a-3 (1-230) x AF177340 (1-1918)

Qy 1 MetAlaSerleuGLYleuGlnLeuValGlyTYrIleleuGLYleuLeuGLYleuLeuGLY 20
Db 520 ATGGCTCTCTTGGCTCCCAACTGTGGGTACATCTTGGGCTTGTGGGCTTTTGGGC 579
Qy 21 ThrLeuValAlaMetLeuLeuProSerTPlyThrSerSerTYrValGlyAlaSerIle 40
Db 580 ACACTGTTGCATGCTGCTCCACAGCTGAAAACAAGTCTTATGTCGTGCGACGATT 639
Qy 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 640 GTACACGAGCTTGGCTTCTCCAAAGGCTCTGATGGAAATGTCCACACACACAGGC 639
Qy 61 IleThrGlnCysAspIleTYrSerThrLeuLeuGLYleuProAlaAspIleGlnAla 80
Db 700 ATCACCAGTGTACATCTATACACCTTCTGGGCTGCTGCTGACATCCAGGCTGCC 759
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 760 CAGGCGATGATGTGACATCCAGTGCATCTCTCCCTGGCTGCATATCTGTGGTG 819
Qy 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
Db 820 GGCATGATGACACATCTTCTCCAGGAATCCCGAACCAACAGAGTGGCGGTAGCA 879
Qy 121 GYGLYVAlPhehelIleuGLYleuLeuGLYPhelIleProValAlaTPaenLeu 140
Db 880 GGTGAGGCTTTTTCATCTTGGAGGCTCTCGGATTCATTCCTGTGGCTGGAACTT 939
Qy 141 HieGLYIleuArgaspPheTYrSerProLeuValProaspSerMetLysPheGluLe 160
Db 940 CATGGATCTTACGGAGACTTCTACTACCACTGGTCTGACAGCATGAATTTGAGATT 999
Qy 161 GYGLYAlaLeuTYrleuGLYIleIleSerSerLeuPheSerLeuIleAlaIle 180
Db 1000 GAGAGGCTCTTACTTGGCATTTTCTTCCTGTTCCTGATAGTGAATCATC 1059
Qy 181 LeuCyPheSerCySerSerGlnArgaspArgSerAsnTYrTraspAlaTYrGlnAla 200
Db 1060 CTCTGCTTTTCCGCTCATCTCCAGAAATCGCTCCAACTACATACGATGCTTACCAAGCC 1119
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
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Qy 221 PheAsnSerTYrSerLeuThrGlyTYrVal 230
Db 1180 TTCAATTCTACAGCTGACAGGGTATGTG 1209

Search completed: December 20, 2004, 16:50:19
Job time: 4306 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 13:30:16 ; Search time 497 Seconds
(without alignments)
2429.310 Million cell updates/sec

Title: US-09-787-677A-3
Perfect score: 1174
Sequence: 1 MASLGQLVGYIIGLLGLG.....PGQPPKVKSEFNSYLTYV 230

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 413486 segs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOEXT=0 -UNIT=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1174	100.0	1400	10	ADJ45986
3	1174	100.0	1400	12	ADP18800
4	1174	100.0	1475	3	AAA37060
5	1174	100.0	1475	4	AAF54296
6	1174	100.0	1475	4	AA621489

7	1174	100.0	1475	4	AA615360	AA615360 cDNA enco
8	1174	100.0	1475	4	AA62097	AA62097 Human PRO
9	1174	100.0	1475	6	AB674417	AB674417 Human CDN
10	1174	100.0	1475	6	ABL88167	ABL88167 Human PRO
11	1174	100.0	1475	6	ABK11089	ABK11089 cDNA enco
12	1174	100.0	1475	6	ABL95656	ABL95656 Human ang
13	1174	100.0	1475	8	ACA81203	ACA81203 Novel hum
14	1174	100.0	1475	8	ACD81580	ACD81580 Human CDN
15	1174	100.0	1475	8	ACA60402	ACA60402 Novel hum
16	1174	100.0	1475	8	ACA03848	ACA03848 cDNA enco
17	1174	100.0	1475	8	ACA58849	ACA58849 cDNA enco
18	1174	100.0	1475	8	ABX89386	ABX89386 DNA enco
19	1174	100.0	1475	8	ACA4025	ACA4025 cDNA enco
20	1174	100.0	1475	8	ACA91289	ACA91289 cDNA enco
21	1174	100.0	1475	8	ACD45188	ACD45188 Human sec
22	1174	100.0	1475	8	ACD42040	ACD42040 Human sec
23	1174	100.0	1475	8	ACA93736	ACA93736 Human CDN
24	1174	100.0	1475	8	ACA67310	ACA67310 cDNA enco
25	1174	100.0	1475	8	ACH66283	ACH66283 Novel hum
26	1174	100.0	1475	8	ACA04269	ACA04269 Human CDN
27	1174	100.0	1475	8	ACD02337	ACD02337 Novel hum
28	1174	100.0	1475	8	ACA89328	ACA89328 Novel hum
29	1174	100.0	1475	8	ACA68965	ACA68965 Novel hum
30	1174	100.0	1475	8	ACA98487	ACA98487 Human PRO
31	1174	100.0	1475	8	ACA63412	ACA63412 cDNA enco
32	1174	100.0	1475	9	ADA46010	ADA46010 Novel hum
33	1174	100.0	1475	9	ADA76441	ADA76441 Human PRO
34	1174	100.0	1475	9	ADB17136	ADB17136 Human CDN
35	1174	100.0	1475	9	ADA19091	ADA19091 Human PRO
36	1174	100.0	1475	9	ADA61714	ADA61714 Homo sapi
37	1174	100.0	1475	9	ADB19499	ADB19499 Novel hum
38	1174	100.0	1475	9	ADB28040	ADB28040 cDNA enco
39	1174	100.0	1475	9	ADA86519	ADA86519 Novel hum
40	1174	100.0	1475	9	ADB16083	ADB16083 Human PRO
41	1174	100.0	1475	9	ADA47869	ADA47869 Human PRO
42	1174	100.0	1475	9	ACH03615	ACH03615 Human sec
43	1174	100.0	1475	9	ACD68331	ACD68331 Novel hum
44	1174	100.0	1475	9	ADA19941	ADA19941 Novel hum
45	1174	100.0	1475	9	ADA67664	ADA67664 Human PRO

ALIGNMENTS

RESULT 1	
AAK97865	
ID AAK97865 standard; cDNA, 1400 BP.	
XX	
AC AAK97865;	
DT 23-SEP-1999 (first entry)	
XX	
DE Human secreted protein encoding cDNA #53.	
XX	
KW Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;	
KW diagnostic; gene therapy; chromosome mapping; secretion vector; ss.	
OS Homo sapiens.	
XX	
PN WO9925825-A2.	
XX	
PD 27-MAY-1999.	
XX	
PF 13-NOV-1998; 98WO-IB001862.	
XX	
PR 13-NOV-1997; 97US-0066677P.	
PR 17-DEC-1997; 97US-0069957P.	
PR 09-FEB-1998; 98US-0074121P.	
PR 13-APR-1998; 98US-0081563P.	
PR 10-AUG-1998; 98US-0096116P.	
PR 04-SEP-1998; 98US-0099273P.	
XX	
PA (GSEST) GENSET.	
XX	

PI Bougueleret L, Duclert A, Dumaz Milne Edwards J;
 XX WPI, 1999-347472/29.
 DR P-PSDB; AAY36181.
 XX Extended cDNAs encoding secreted proteins.
 XX Claim 1, Page 254-255, 307pp; English.
 XX
 CC AAX97813-X97906 represent extended cDNA's which encode novel human
 CC secreted proteins (see AAY36129-Y36222) and which have cytostatic,
 CC thrombotic and osteopathic activity. The extended cDNAs can be used to
 CC express secreted proteins or parts of them or to obtain antibodies
 CC capable of binding to the secreted proteins. They may also be used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC Uses also include design of expression vectors and secretion vectors
 XX
 SQ Sequence 1400 BP; 326 A; 392 C; 346 G; 336 T; 0 U; 0 Other;

Alignment Scores:
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 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-787-677a-3 (1-230) x AAX97865 (1-1400)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 Db 36 ATGGCCCTCTTGCCCTTCCCAACTGTGGGCTACATCCAGGCTTCTGGGGCTTTGGGC 95
 QY 21 ThrIleuValAlaMetLeuLeuProSerTrrIyThrserserTyrValGlyAlaSerIle 40
 Db 96 ACATGCTTGCCACAGCTGCTCCCGAGCTGGAACAAAGTTCTTATGTCGGGCGACGATT 155
 QY 41 ValThrAlaValGlyPheSerTyrGlyLeuTrrPheGluCysAlaTrrHisSerThGly 60
 Db 156 GTGACACAGATTGGCTTCTCCAGAGGCTCTGAGTGAATGTCCACACACAGACAGGCC 215
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 Db 216 ATGACCCAGTGTGACATCTATAGCACCTTCTGGGCGCTGCCGCTGACATCAGGCTGCC 275
 QY 81 GlnAlaMetIleValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 276 CAGGCCATGATGGACATCCAGCAATCTCCCTGGGCTTCATTTCTGTGGTG 335
 QY 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaValAspArgValAlaValAla 120
 Db 336 GGCAATGATGACAGACTTCTGCGCAGAAATCCGAGCCAAAGACAGATGGCGGTAGCA 395
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrrAsnLeu 140
 Db 396 GGTGGAGCTTTTTCATCTTGAGAGGCTCTCTGGAGTTCATCTGTTGGCTGGAATCTT 455
 QY 141 HisGlyIleLeuAlaGaaPheTyrSerProLeuValProAspSerMetIyPheGluIle 160
 Db 456 CATGGAGTCTTACCGGACTTCTACTCACTGTGTGCTGACACATGAATTTGAAATT 515
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 Db 516 GGAAGAGCTCTTTCATCTGGGCAATTTCTTCCCTGTTCTCCGATGACGGAATCATC 575
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 576 CTCTGCTTTTCTCTCATCCAGAAATGCTCCCAACTCTAGATGCTTACCAAGCC 635
 QY 201 GlnProLeuAlaTrrArgSerSerProArgProGlyGlnProPolylValValSerGlu 220
 Db 636 CAACCTCTTGCCACAGAGCTCTCCAAAGGCTGTGATCACTCCCAAAAGTCAGAGTGAG 695

QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 696 TTCAATTCCTACAGCTGACAGGGTATGTG 725
 RESULT 2
 ID ADJ45986 standard; cDNA, 1400 BP.
 XX
 AC ADJ45986;
 XX
 XX 06-MAY-2004 (first entry)
 DE Novel human secreted protein-related cDNA sequence SeqID139.
 XX
 KW secreted protein; upstream regulator; gene therapy; protein purification;
 KW protein synthesis; chromosomal mapping; individual identification;
 KW forensic; hereditary disease; drug reaction; immunoassay;
 KW epitope mapping; vaccine; immune system regulation;
 KW haematopoietic system; tissue growth; reproductive hormone;
 KW cell migration; blood clotting; receptor/ligand interaction;
 KW adhesion molecule; assisted drug delivery;
 KW human glial maturation factor gamma-2; neurite outgrowth;
 KW neurite resprouting; human; gene; ss.
 OS Homo sapiens.
 PN US2003144490-A1.
 XX
 XX 31-JUL-2003.
 PD
 XX 10-DEC-2002; 2002US-00319763.
 PF
 XX 13-NOV-1997; 97US-0066677P.
 PR 17-DEC-1997; 97US-0069957P.
 PR 09-FEB-1998; 98US-0074121P.
 PR 13-APR-1998; 98US-0081563P.
 PR 10-AUG-1998; 98US-0096116P.
 PR 04-SEP-1998; 98US-0099273P.
 PR 13-NOV-1998; 98US-00191997.
 PR 15-SEP-2000; 2000US-00663600.
 XX
 XX (EDWA/) EDWARDS J D M.
 PA (DUCL/) DUCLEERT A.
 PA (BOUG/) BOUGUELERET L.
 XX
 PI Edwards JDM, Duclert A, Bougueleret L;
 XX WPI, 2003-851788/79.
 DR P-PSDB; ADJ46033.
 XX
 PT New nucleic acid encoding secreted human polypeptides, useful e.g. in
 PT gene therapy or diagnosis, also encoded proteins, potential therapeutic
 PT agents.
 XX
 PS Claim 3; SEQ ID NO 139; 269pp; English.
 XX
 CC This invention relates to novel purified isolated polynucleotides which
 CC comprise a sequence that encodes at least 10 amino acids (aa) from any of
 CC 48 secreted polypeptide sequences, given in the specification, or
 CC fragments of polypeptides encoded by human cDNA contained in the
 CC corresponding deposited clone. The DNA sequences of the invention encode
 CC secreted proteins (or their fragments) and can be used to
 CC identify/isolate upstream regulators, potentially useful in gene therapy
 CC or protein purification, by controlling protein synthesis, as probes for
 CC chromosomal mapping, identification of individuals, and for diagnosis or
 CC forensic, for example identifying genes associated with hereditary
 CC diseases or drug reactions, for recombinant expression of the encoded
 CC proteins or, where the DNA sequence encodes a signal peptide, for
 CC directing secretion of heterologous polypeptides. Polypeptides encoded by
 CC the DNA sequences of the invention can be used to raise antibodies,
 CC useful for detecting the polypeptide, as (ant)agonists, or for preparing
 CC anti-idiotypic antibodies, as tags in for example immunoassays, epitope
 CC mapping or vaccines, also as molecular weight markers, to screen for

CC agents with biological activity and as therapeutic agents with.
CC potentially, a very wide range of activities, for example regulation of
CC the immune or haematopoietic systems, tissue growth, reproductive
CC hormones, cell migration, blood clotting or receptor/ligand interaction,
CC also as adhesion molecules for assisted drug delivery. A typical isolated
CC sequence is human glial maturation factor gamma-2, which stimulates
CC neurite outgrowth and resprouting. The present sequence is a cDNA
CC sequence which encodes a human secreted protein of the invention.
XX
SQ Sequence 1400 BP; 326 A; 392 C; 346 G; 336 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,4e-122	Length:	1400
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-787-677a-3 (1-230) x ADP18800 (1-1400)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB 36 ATGGCCCTCTTGCGCTCCAACTGTGGGCTACATCTTAGGCTTGGGGCTTTGGGC 95
QY 21 ThrLeuValAlaMetLeuLeuProSerTTrpLysThrSerSerTyrValGlyAlaSerIle 40
DB 96 ACACGTGGTCCATGCTGCTCCCACTGGAGAAACAAGTTCTTATGCGGTGCCAGCATT 155
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
DB 156 GTACACGACATTTGGCTTCTCCAAAGGCTCTGATGAAATGTGCCACACACAGACAGGC 215
QY 61 IleThrGlnCysAspIleYrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
DB 216 ATCACCAGGTGATCATCTATAGACACCTTCTGGGCTGCCGCTGACATCCAGGCTGCC 275
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 276 CAGGCGCATGATGTGACATCAGTGAATCTCCCTGCGCTGCATATCTCTGTGGTG 335
QY 101 G1MetArgCysThrValPheCysGlnG1SerArgAlaValAspArgValAlaValAla 120
DB 336 GGCATGATGATGACAGCTTCTTCCAGGAATCCGACGCCAAAGACAGATGGCGGTAGCA 395
QY 121 G1GlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaATPAsnLeu 140
DB 396 GGTGAGTCTTTTTCATCTTGGAGGCTCTGGGATTCATTCCTGTTGCTGGAACTT 455
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 456 CATGGAGTCTTACGGGACTTCTACTCACACTGGTGTCTTACAGCATGAATTTGAAATT 515
QY 161 G1GlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
DB 516 GAGAGGCTTTTAACTTGGGATTAATTTCTCCCTGTTCCCTGATAGCTGGAGATATC 575
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
DB 576 CTCTGCTTTTCCGCTCATCCAGAAATCGCTCCAACTACTACATGATGCTTACCAAGCC 635
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 636 CAACCTCTTGCCCAAGAGACTCTCCCAAGGCTGGTCAACTCCCAAGTCAAGAGAGTGA 695
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 696 TTCAATTCTTACAGCTGACAGGATATGTG 725

RESULT 3
ADP18800
ID ADP18800 standard; cDNA; 1400 BP.
XX

AC ADP18800;
XX
XX 26-AUG-2004 (first entry)
XX
XX Human secreted polynucleotide #56.
DE Human secreted polynucleotide #56.
XX
XX Human, secreted protein; gene; ss; genetic disease.
OS Homo sapiens.
XX
XX US2004110939-A1.
XX
XX 10-JUN-2004.
XX
XX 15-OCT-2001; 2001US-00978360.
XX
XX 17-DEC-1998; 98WO-IB002122.
XX 09-FEB-1999; 99WO-IB000282.
XX 21-JUN-2000; 2000WO-IB000951.
XX 15-SEP-2000; 2000US-00663600.
XX
XX (BEST) GENSET SA.
XX
XX Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;
PI Ductert A;
XX
XX WPI; 2004-440404/41.
XX
XX P-PSDB; ADP19205.
XX
XX New isolated polynucleotide encoding secreted polypeptide, useful for
PT gene therapy, or in diagnostic procedures to identify individuals having
PT genetic diseases resulting from abnormal expression of the genes.
XX
XX
XX Claim 1; SEQ ID NO 56; 113pp; English.

CC The invention relates to human cDNA sequences that encode human secreted
CC proteins. The invention also relates to an antibody that specifically
CC binds to a polypeptide of the invention and a method of binding the
CC polypeptide to an antibody. The polynucleotides are useful for expressing
CC the entire secreted proteins which they encode and for distinguishing
CC human tissues and cells from non-human tissues and cells, and for
CC distinguishing between human tissues and cells that do or do not express
CC the polynucleotides comprising the cDNAs. The polynucleotides and
CC polypeptides are useful in forensic procedures or diagnostic procedures
CC to identify individuals with genetic diseases resulting from abnormal
CC expression of the genes corresponding to the cDNAs. The sequences are
CC also useful in gene therapy to control or treat genetic diseases. This
CC sequence represents a human secreted polynucleotide of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
XX

SQ Sequence 1400 BP; 326 A; 392 C; 346 G; 336 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,4e-122	Length:	1400
Score:	1174.00 <td>Matches:</td> <td>230</td>	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-787-677a-3 (1-230) x ADP18800 (1-1400)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB 36 ATGGCCCTCTTGCGCTCCAACTGTGGGCTACATCTTAGGCTTGGGGCTTTGGGC 95
QY 21 ThrLeuValAlaMetLeuLeuProSerTTrpLysThrSerSerTyrValGlyAlaSerIle 40
DB 96 ACACGTGGTCCATGCTGCTCCCACTGGAGAAACAAGTTCTTATGCGGTGCCAGCATT 155
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60

Db 156 GTGACAGACATTGGCTTCTCAAGAGGCTCTGGATGTAATGTGCACACAGACAGCGGC 215
Qy 61 ILeThrGlnCysAspIleTySerThrLeuGlyLeuProAlaAspIleGlnAla 80
Db 216 ATCACCAGTGTGACATCTATAGCACCTTCTGGGCTGCGCCGTGACATCCAGCTGCC 275
Qy 81 GAlaIleMetValIThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 276 CAGGCCATGATGGTGAATCCAGTCAATCTCTCCCTGGCTGCTGATTTCTGTGTG 335
Qy 101 G1yMeArGcYsThrValIheCyGlnGlnSerArgAlaIyAspArgValAlaValAla 120
Db 336 GCGATGAGATGCAAGCTTCTGCGAGAAATCCGAGCAAAAGACAGTGGCGTGC 395
Qy 121 G1yG1yValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaITrPAnLeu 140
Db 396 GGATGAGCTTTTTCATCTTGGAGGCTCTCGGAGATTCATCTGTGCTGGATCTT 455
Qy 141 H1eG1yIleLeuArgAspPheTySerProLeuValProAspSerMetIyPheGluIle 160
Db 456 CATGGATCTTACCGGACTTCTACTACACACTGTGCTGACAGCATGAATTTGAGATT 515
Qy 161 G1yG1uAlaLeuTyLeuGlyIleIleSerSerLeuPheSerIleuIleAlaGlyIle 180
Db 516 GAGAGGCTCTTACTTGGGATATTCTTCCCTGTTCTCCGTGATGCGATCATC 575
Qy 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAnTyTyAspAlaITyGlnAla 200
Db 576 CTCTGCTTTCTCTCTCATCCAGAAATGCTCAACTGATGATGCTTACCAAGCC 635
Qy 201 GlnProLeuAlaIThrArgSerSerProArgProGlyGlnProValIySerGlu 220
Db 636 CAACCTCTTGCACAGAGCTCTCCAGAGCTGTCACTCCCAAGTCAAGAGTGA 695
Qy 221 PheAnSerTySerLeuThyGlyTyVal 230
Db 696 TTCAATTCCTACAGCTGACAGGATGTG 725
RESULT 4
AAA37060
ID AAA37060 standard; cDNA; 1475 BP.
XX
AC AAA37060;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1356 (UNQ705) cDNA sequence SEQ ID NO:133.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
XX transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
PD 09-MAR-2000.
XX
XX 01-SEP-1999; 99WO-USO20111.
XX
PR 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 03-SEP-1998; 98US-0099536P.
PR 03-SEP-1998; 98US-0099566P.
PR 03-SEP-1998; 98US-0099598P.
PR 03-SEP-1998; 98US-0099602P.
PR 03-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.

PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 22-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101478P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101745P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102020P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 30-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103499P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105002P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105265P.
PR 26-OCT-1998; 98US-0105683P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.

PR 27-OCT-1998; 98US-0105882P.
 PR 27-OCT-1998; 98US-0106062P.
 PR 28-OCT-1998; 98US-0106023P.
 PR 28-OCT-1998; 98US-0106029P.
 PR 28-OCT-1998; 98US-0106030P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106178P.
 PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106384P.
 PR 29-OCT-1998; 98US-0108500P.
 PR 30-OCT-1998; 98US-0106464P.
 PR 03-NOV-1998; 98US-0106465P.
 PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
 XX WPI; 2000-237871/20.
 DR P-PSDB; AAY99378.
 XX
 PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO polypeptides, useful for screening of potential peptide or small
 PT molecule inhibitors of the relevant receptor/ligand interactions.
 XX
 PS Claim 2; Fig 77; 773pp; English.
 XX
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding them have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR
 CC primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention
 XX
 SO Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-787-677A-3 (1-230) x AAA37060 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValIGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly 20

DB 122 ATGGCTCTCTTGGCTCCAACTTGCGGCTGACATCTAGGCTTGGGCTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTPVThrSerSerTyrValGlyAlaSerIle 40
 DB 182 ACACGTGTGTCATGCTGCTCCCACTGGAAACAAAGTTCTTATGCGGTGCAGCATT 241
 QY 41 ValThrAlaValIGlyPheSerIlysglyLeuTTPMeGluCysAlaIleThrIleSerThrIly 60
 DB 242 GTACACGACAGTTGGCTTCCCAAGGGCTCTGGATGGAATGTCCACACACACACAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaIle 80
 DB 302 ATCACCAGTGTACATCTATACACCTTCTTGAGGCTGCCCTGCATCTCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 DB 362 CAGGCCATGATGTGTGACATCAGTGCATCTCTCCCTGGCTGCATTTATCTGTGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaValAla 120
 DB 422 GGCATGAGATGCACAGCTCTTCCCAAGATCCCGAGCCAAAGACAGAGTGGCGTAGCA 481
 QY 121 GIGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTTPAenLeu 140
 DB 482 GGTGAGCTCTTTCATCTTGAAGGCTCTGGATTCATCTCTGTGCTTGGATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 DB 542 CATGGATCTTACGGGACTTCTACCTCACACCTGCTGCTGACGATGAATTTGAGATT 601
 QY 161 GIGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 DB 602 GGAGAGGCTCTTACCTTGGGCAATTATTTCTTCCCTGTCTCCCTGATGATCATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAspArgSerAspTyrTyrAspAlaTyrGlnAla 200
 DB 662 CTCTGCTTCTTCTGCTCATCTCCAGAAATGCTCCAACTACTACATGCTCTCCAAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValLysSerGlu 220
 DB 722 CAACCTCTTGCCCAAGAGAGCTCTCCAGGCTGTGCACTCTCCAAAGTCAAGAGTAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 782 TTCAAATCTTACAGCTGACAGGATATGTG 811

RESULT 5

ID AAF54296 standard; DNA; 1475 BP.

XX AAF54296;

AC 02-APR-2001 (first entry)

DT DNA encoding protein of the invention #39.

DE Secreted; transmembrane; gene therapy; ss.

XX Unidentified.

PN WO200078961-A1.

PD 28-DEC-2000.

PF 18-FEB-2000; 2000MO-US004342.

XX 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-014758P.

PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99MO-US020111.

PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99MO-US028313.

PR 02-DEC-1999; 99MO-US028551.
 PR 16-DEC-1999; 99MO-US030095.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000376.
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
 PI Williams PM, Wood WI;
 DR WPI; 2001-071395/08.
 XX
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.
 XX
 PS Claim 2; Fig 77; 787pp; English.
 XX
 CC The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of anti-
 CC sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1 Site-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-787-677a-3 (1-230) x AAF54296 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
 Db 122 ATGGCCCTCTTGGCTCAACCTGTGGGCTACATCTCAGGCTTGTGGGCTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrIleThrSerSerTyrValGlyAlaSerIle 40
 Db 182 ACACTGGTGCACAGCTGCTCCAGCTGGAACCAAGTTCTTATGTCGGGCGACGACATT 241
 QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTyrMetGluCysAlaThrAlaSerThrGly 60
 Db 242 GTGACACAGCTTGGCTTCTCCAGGGCTCTGATGGAATGTGCACACACAGACAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
 Db 302 ATGACCCAGCTGACATCTATAGCACCTTCTGGGCTGCGCGCTGACATCAGGCTGCC 361
 QY 81 GlnAlaMetLeuValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 362 CAGGCCATGATGGAGACATCCAGTGCATCTCCCTCGGCTCATTTATCTCTGGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerGlnAlaValAspArgValAlaValAla 120
 Db 422 GGCATGAGATGCACAGCTTCTTCCAGGAATCCGAGCCAAAGACAGATGCGCGTACCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrAsnLeu 140
 Db 482 GGTGAGATCTTTTCATCTTGAAGGCTCTCGGATTCATTTCTGTTGCTGGATCTT 541
 QY 141 HisGlyIleLeuAlaGlyAspPheTyrSerProLeuValProAspSerMetValPheGluIle 160
 Db 542 CATGGGATCTCCACGAGCTTCTACTACACACTGGTGCTGACACATGAAATTTGAGATT 601
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180

Db 602 GGAGAGCTCTTACTTGGGCACTTATTTCTCCCTGTCTCCCTGATAGCTGAATCATC 661
 QY 181 LeuCyPheSerCysSerSerGlnAlaGlnAlaSerAsnTyrTyrPheAlaTyrGlnAla 200
 Db 662 CTCTGCTTTTCCCTGCATCTCCAGAGAAATGCTCCAACTACTACGATGCTTCCAGGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValIysSerGlu 220
 Db 722 CAACCTTCTCCACAGAGCTTCTCCAGGCTGTCTCACTCCCAAGTCAAGAGTGAAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 782 TTCATTCCTACAGCTGACAGGATATGTG 811

RESULT 6
 AAS21489
 ID AAS21489 standard; cDNA; 1475 BP.
 XX
 AC AAS21489;
 XX
 AC 24-OCT-2001 (first entry)
 XX
 DT Human cDNA sequence encoding for PRO1356 polypeptide.
 XX
 DE Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumour necrosis factor- α ; TNF- α ; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIa; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000MO-US032678.
 XX
 PR 01-DEC-1999; 99MO-US028301.
 PR 01-DEC-1999; 99MO-US028634.
 PR 02-DEC-1999; 99MO-US028551.
 PR 02-DEC-1999; 99MO-US028564.
 PR 02-DEC-1999; 99MO-US028565.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99MO-US030095.
 PR 20-DEC-1999; 99MO-US030911.
 PR 20-DEC-1999; 99MO-US030999.
 PR 30-DEC-1999; 99MO-US031243.
 PR 30-DEC-1999; 99MO-US031274.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000277.
 PR 06-JAN-2000; 2000MO-US000376.
 PR 11-FEB-2000; 2000MO-US003565.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 24-FEB-2000; 2000MO-US004914.
 PR 24-FEB-2000; 2000MO-US005004.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000MO-US006319.
 PR 15-MAR-2000; 2000MO-US006884.
 PR 20-MAR-2000; 2000MO-US007377.
 PR 21-MAR-2000; 2000MO-US007532.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 11-AUG-2000; 2000MO-US022031.

PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023528.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 10-NOV-2000; 2000MO-US030873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Berejini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WP1; 2001-408281/43.
 P-PSDB; AAU2417.
 XX
 PT Isolated , secretary and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 XX
 PS Claim 3; Fig 491; 813pp; English.
 XX
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes, or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-787-677A-3 (1-230) x AAS21489 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
 Db 122 ATGGCCCTCTTGGCTCCCACTTGTGGCTGATCTCTAGGCCCTTCTGGGGCTTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValGlyAlaSerIle 40
 Db 182 ACACGTGGTCCATGCTGCTCCCACTGAGAAACAAGTCTTATGTCGGTCCAGCAATT 241
 QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTyrPheGlnCysAlaThrHisSerThrGly 60
 Db 242 GTGACAGCACTTGGCTTCTCCCAAGGGCTCTGATGATGAATGTGCACACAGCAGCAGC 301
 QY 61 IleThrGlnGlyAspIleTyrSerThrLeuGlnGlyLeuProAlaAspIleGlnAlaAla 80
 Db 302 ATACACCAAGGTACATCTATAGCACCTTCTGGGCTGTGCCGTGACATCCAGGCTGCC 361
 QY 81 GluAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 362 CAGGCCATGATGTGACATCCAGTGCATCTCTCTGCGCTGCAATTATCTCTGTGGTG 421

QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
 Db 422 GGCATGAGATGACACAGCTCTTCTGCGAGGAATCCGACCAAGACAGAGTGGCGGTAGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlnGlyLeuLeuGlyPheIleProValAlaTyrAsnLeu 140
 Db 482 GGTGAGCTCTTTTCATCTTGAGGCTCTGAGATTCATCTGTGGCTGGAACTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 Db 542 CATGGATCCTTAGCGGACTTCTACTACCACTGGTGTGCTGACAGCATGAATTTGAATT 601
 QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 Db 602 GGAAGGCTCTTTACTTGGGCAATTAATTTCTCTGTTCCCTCGATGATGGAATCATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAntTyrTyrAspAlaTyrGlnAla 200
 Db 662 CTGCTCTTTCGCTCATCCAGAGAAATGCTCCAACTACTAGATGCTTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
 Db 722 CAACCTTCCCAACAGAGACTCTCCAGGCTGTGTCAACTCCCAAGTCAAGATGAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 782 TTCAATTCCTACAGCTGACAGGATGATGTG 811
 RESULT 7
 AAS15360
 ID AAS15360 standard; cDNA; 1475 BP.
 XX
 AC AAS15360;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE cDNA encoding human PRO1356 polypeptide.
 XX
 KW Human; PRO1356; clone DNA64886-1601; immune-related disorder;
 KW inflammatory disorder; infectious disorder; immunodeficiency disorder;
 KW autoimmune disorder; renal disease; demyelinating disease; skin disease;
 KW neoplasia; transplantation associated disease; gene therapy;
 KW immunosuppressive; anti-inflammatory; antidiabetic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 122..814
 FT /*tag= a
 FT /product= "PRO1356 polypeptide"
 FT /*tag= b
 FT mat_peptide 194..811
 FT /*tag= c
 FT
 PN WO200166740-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 01-MAR-2001; 2001MO-US006666.
 XX
 XX 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191015P.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 24-AUG-2000; 2000MO-US023528.
 PR 01-DEC-2000; 2000MO-US032678.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Eaton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL,
 PI Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WP1: 2001-625876/72.
 DR P-PSDB; AAU09178.
 XX Nucleic acids encoding PRO polypeptides, useful for detecting and
 PT treating immune related diseases and disorders in mammals including
 PT autoimmune diseases, inflammatory diseases and asthma.
 XX
 PS Claim 2; Fig 1; 122bp; English.
 XX
 CC The present invention relates to the isolation of 9 novel human PRO
 CC polypeptides (AAU09178-AAU09186) and the cDNA sequences encoding them.
 CC The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,
 CC PRO3151, PRO4322, PRO9964, PRO10008 and PRO19598. The cDNA sequences
 CC encoding these PRO polypeptides have been designated as clones DNA64886-
 CC 1601, DNA64903-1553, DNA84318-2520, DNA87997, DNA89273, DNA82223-2567,
 CC DNA96973, DNA101921 and DNA145887 respectively. Compositions (e.g.
 CC vaccines) containing PRO polypeptides and methods of using these
 CC compositions are useful in the treatment and diagnosis of immune-related
 CC disorders. Such disorders include immune-mediated inflammatory disorders
 CC (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g.
 CC diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis),
 CC immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g.
 CC rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis),
 CC demyelinating diseases of the peripheral or central nervous system (e.g.
 CC Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact
 CC dermatitis), neoplasias and transplantation associated diseases. The
 CC polynucleotide sequences of the invention may be used in gene therapy.
 CC AAU15360-AAU15368 represent cDNA sequences encoding for the novel human
 CC PRO polypeptides of the invention
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 1,51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-787-677A-3 (1-230) x AAU15360 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 Db 122 ATGGCCCTCTTGAGCTTCACTGTGGCTACTTCTAGGCTTCTGGGCTTTGGGC 181
 QY 21 ThrIleuValAlaMetLeuLeuProSerTyrIleThrSerSerTyrValGlyAlaSerIle 40
 Db 182 ACACGTGTTGCGCATGTGCTCCAGCTGGAAACAAATTCTTATGTCGGTCCAGCAT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThrGly 60
 Db 242 GTGACACAGCTGGCTTCTCCAGGGCTCTGAGATGTGCACACACAGCAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
 Db 302 ATCACCCAGTGTGATCTATAGCACCTTGTGGCCCTGCGGTGACATCAGGCTGCC 361
 QY 81 GlnAlaMetMetValIleThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 Db 362 CAGGCCATGATGTGACATCCAGTGCATCTCTCCGCTGCATATCTCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaValAspArgValAlaValAla 120
 Db 422 GGCATGTAGATGCACAGTCTTCTGCCAGGAATCCGAGCCAAAGACAGTGGCGTAGCA 481
 QY 121 GlyValValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrAsnLeu 140
 Db 482 GGTGAGTCTTTTCACTCTTGAGGCTCTCTGGGATTCATCTCTGTGGCAATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLeuPheGluIle 160

Db 542 CATGGATCTTACGGGACCTTCTACTCACCATGTGCTTCAGACATGAATTTGAGATT 601
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 Db 602 GGAGAGGCTTTTACTTGGGCATTATTCTTCCCTGTCTCCGTAGTGGATCATC 661
 QY 181 LeuCySPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 662 CTCGCTTTTCTGCTCATATCCAGAGAAATCGCTCCAACTACATGCTCCAGAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValIleSerGlu 220
 Db 722 CAACCTTCTCCCAAGAGACTCTCCAGGCTGTGTCACCTCCCAAGTCAAGAGTAG 781
 QY 221 PheAsnSerTyrSerLeuTyrGlyTyrVal 230
 Db 782 TTCATTTCTTACAGGCTTCAGACGGGTATGTG 811
 RESULT 8
 ID AAF92097 standard; cDNA; 1475 BP.
 XX
 AC AAF92097;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Human PRO1356 cDNA.
 XX
 KW Human; PRO protein; mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200116318-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 24-AUG-2000; 2000MO-US023328.
 XX
 PR 01-SEP-1999; 99MO-US020111.
 XX
 PR 15-SEP-1999; 99MO-US021090.
 XX
 PR 07-DEC-1999; 99US-0169495P.
 XX
 PR 09-DEC-1999; 99US-0170262P.
 XX
 PR 11-JAN-2000; 2000US-0175481P.
 XX
 PR 18-FEB-2000; 2000MO-US004341.
 XX
 PR 18-FEB-2000; 2000MO-US004342.
 XX
 PR 22-FEB-2000; 2000MO-US004414.
 XX
 PR 01-MAR-2000; 2000MO-US005601.
 XX
 PR 03-MAR-2000; 2000US-0187202P.
 XX
 PR 21-MAR-2000; 2000US-0191007P.
 XX
 PR 30-MAR-2000; 2000MO-US008439.
 XX
 PR 25-APR-2000; 2000US-0199397P.
 XX
 PR 22-MAY-2000; 2000MO-US014042.
 XX
 PR 05-JUN-2000; 2000US-0209832P.
 XX
 PA (GERTH) GENENTECH INC.
 XX
 XX Earon DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 XX
 DR WP1: 2001-183260/18.
 XX
 DR P-PSDB; AAB87565.
 XX
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 PT biology, including use as hybridization probes, and in chromosome and
 XX gene mapping.
 PS
 PS Claim 2; Fig 79; 278bp; English.
 XX
 CC The present sequence is the coding sequence for a human PRO polypeptide
 CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
 CC antagonists or anti-PRO antibodies are useful for preparation of a
 CC medicament useful in the treatment of a condition which is responsive to
 CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO

CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping

XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,51e-122	Length:	1475
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-787-677a-3 (1-230) x AAF92097 (1-1475)

QY	1	MetAlSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly	20
DB	122	ATGGCTCTCTTGGCTCCAACTTGTGGCTTACATCTTACGGCTTCTGGGGCTTTGGGC	181
QY	21	ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle	40
DB	182	ACACGTGTGCCATGCTGCTCCCAAGCTGGAACAAAGTTCTTATGCGGTGCACGATT	241
QY	41	ValThrAlaValGlyPheSerLysGlyLeuTrpMetGlyCysAlaTrpHisSerThrGly	60
DB	242	GTGACGACGATGGCTTCTCCAAAGGCTCTGATGGAATGGTCCACACACACACAGGC	301
QY	61	IleThrGlyCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla	80
DB	302	ATACCCAGTGTACATCTTACGACCTTCTGGGCTGCGCGTGCATCCAGGCTGCC	361
QY	81	GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal	100
DB	362	CAGGCATGATGTGATCATCAGTCAATCTCTCCCTGGCGTCGATTATCTGTGGTG	421
QY	101	GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaVal	120
DB	422	GGCATAGAGACAGCTTCTCCAGAGATCCCGACCAAGACAGAGTGGCGTAGCA	481
QY	121	GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu	140
DB	482	GGTGGATCTTTTTCATCTTGAAGGCTCTCGGATTCATCTGTGCTGGATCTT	541
QY	141	HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle	160
DB	542	CATGGATCTTACGGGACTTCTACTCACACTGTGCTGACAGCAGAAATTTGAGATT	601
QY	161	GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle	180
DB	602	GGAGAGGCTCTTACCTGGGCAATTATTTCTCCCTGTTCTCCGTAGTGGATCATC	661
QY	181	LeuCysPheSerCysSerSerGlnArgAsnArgSerSerTrpTyrAspAlaTyrGlnAla	200
DB	662	CTCTGCTTTTCCGCTCATCTCCAGAGAAATGGCTCCCACTACGATGCTTCCAGGCC	721
QY	201	GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu	220
DB	722	CAACCTCTTGCCACAGAGAGCTTCCAGAGCCTGGTAACTCTCCAAAGTCAGAGAGGAG	781
QY	221	PheAsnSerTyrSerLeuThrGlyTyrVal	230
DB	782	TTCAATTCTTACAGCTGACAGGATGTTGTG	811

RESULT 9

ABST74417 standard; cDNA; 1475 BP.

AC ABST74417;

DT 10-DEC-2002 (first entry)

DE Human cDNA encoding secreted/transmembrane protein PRO1356.

XX Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;

KW antiarthritic; osteopathic; sports-related joint problem;

KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX Homo sapiens.

PN US2002119130-A1.

PD 29-AUG-2002.

PF 06-DEC-2001; 2001US-00006867.

XX	29-OCT-1997;	97US-0063435P.
XX	29-OCT-1997;	97US-0064215P.
XX	22-APR-1998;	98US-0082797P.
XX	29-APR-1998;	98US-0083495P.
XX	15-MAY-1998;	98US-0085579P.
XX	02-JUN-1998;	98US-0087759P.
XX	04-JUN-1998;	98US-0088021P.
XX	04-JUN-1998;	98US-0088029P.
XX	10-JUN-1998;	98US-0088030P.
XX	10-JUN-1998;	98US-0088734P.
XX	10-JUN-1998;	98US-0088740P.
XX	10-JUN-1998;	98US-0088811P.
XX	10-JUN-1998;	98US-0088824P.
XX	10-JUN-1998;	98US-0088825P.
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XX	16-JUN-1998;	98US-0089514P.
XX	17-JUN-1998;	98US-0089553P.
XX	19-JUN-1998;	98US-0089952P.
XX	22-JUN-1998;	98US-0090246P.
XX	24-JUN-1998;	98US-0090444P.
XX	25-JUN-1998;	98US-0090688P.
XX	25-JUN-1998;	98US-0090696P.
XX	26-JUN-1998;	98US-0090862P.
XX	02-JUL-1998;	98US-0091628P.
XX	10-AUG-1998;	98US-0096012P.
XX	17-AUG-1998;	98US-0096757P.
XX	18-AUG-1998;	98US-0096949P.
XX	18-AUG-1998;	98US-0096959P.
XX	26-AUG-1998;	98US-0097954P.
XX	26-AUG-1998;	98US-0097971P.
XX	01-SEP-1998;	98US-0097979P.
XX	10-SEP-1998;	98US-0098749P.
XX	10-SEP-1998;	98US-0099741P.
XX	10-SEP-1998;	98US-0099763P.
XX	10-SEP-1998;	98US-0099792P.
XX	10-SEP-1998;	98US-0099812P.
XX	10-SEP-1998;	98US-0099815P.
XX	16-SEP-1998;	98US-0100627P.
XX	16-SEP-1998;	98US-0100662P.
XX	16-SEP-1998;	98US-0100683P.
XX	17-SEP-1998;	98US-0100684P.
XX	17-SEP-1998;	98US-0100930P.
XX	22-SEP-1998;	98US-0101279P.
XX	23-SEP-1998;	98US-0101475P.
XX	24-SEP-1998;	98US-0101738P.
XX	24-SEP-1998;	98US-0101743P.
XX	24-SEP-1998;	98US-0101916P.
XX	30-SEP-1998;	98US-0102570P.
XX	06-OCT-1998;	98US-0103449P.
XX	08-MAR-1999;	99MO-US005028.
XX	14-MAY-1999;	99MO-US010733.
XX	02-JUN-1999;	99MO-US012252.
XX	01-SEP-1999;	99MO-US020111.
XX	15-SEP-1999;	99MO-US021090.
XX	15-SEP-1999;	99MO-US021194.
XX	22-DEC-1999;	99MO-US030720.
XX	18-FEB-2000;	2000MO-US004341.

PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 10-NOV-2000; 2000MO-US030873.
 PR 01-DEC-2000; 2000MO-US032378.
 PR 20-DEC-2000; 2000MO-US034956.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 01-MAR-2001; 2001MO-US006666.
 PR 30-MAY-2001; 2001MO-US017443.
 PR 01-JUN-2001; 2001MO-US017800.
 PR 20-JUN-2001; 2001MO-US019692.
 PR 29-JUN-2001; 2001MO-US021066.
 PR 09-JUL-2001; 2001MO-US021735.
 XX
 PA (GETH) GENENTECH INC.
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX P-PSDB; ABG95890.
 DR WPI: 2002-731348/79.
 PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.
 XX
 PS Claim 2; Fig 79; 399pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, C/G, H or I or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis
 CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence encodes a novel secreted or transmembrane protein of the

CC invention
 XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 1,51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-787-677a-3 (1-230) X ABS74417 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
 Db 122 ATGGCCCTCTTGCCCTCCCAAGCTGGGGCTTAACCTCCTAGCCCTTCGGGGCTTTGGGC 181
 QY 21 ThrIleuValAlaMetLeuLeuProSerTrpIleThrSerSerTyrValGlyAlaSerIle 40
 Db 182 ACACTGTTGCCATGCTGCTCTCCCACTGGAGAAACAAAGTCTTATGTCGGTCCAGCATT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGluCysAlaTrpHisSerThrGly 60
 Db 242 GTGACAGACAGTGGCTTCTCCAAAGGCGCTCGATGGAATGTCACACACAGACAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 Db 302 ATCCACCAAGGTGACATCTATAGACCTTCTGGCTGCTGCTGACATCCAGGCTGCC 361
 QY 81 GlAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 362 CAGGCCATGATGTGATGATCATCATGCAATCTCTCTGCTGCTGCTGATATCTCTGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnIleSerArgAlaValAspArgValAlaValAla 120
 Db 422 GGATGAGATGACAGACTTCTGCTCCAGGAATCCGACCAAGACAGAGTGGCGGTGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleProAspLeu 140
 Db 482 GTGTGAATCTTTTTCATCTTGAGGCTCTGAGGCTCTGATTCATTTCTGTGCTGGAACTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetCysPheGluIle 160
 Db 542 CATGGATCTCAGGAGCTTCTACTACCACTGCTGCTGACAGCAAGAAATTTGAAATT 601
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 Db 602 GGAAGGCTCTTACTTGGGCAATATTTCTTCCCTGTTCTCCGATGAGCTGGAATCATC 661
 QY 181 LeuCyAspSerCysSerSerGlnArgAsnArgSerLeuTyrTrpAlaIleTyrGlnAla 200
 Db 662 CTCGCTTTTCTGCTCATCTCCAGAAATCGCTCCAACTACATGATGCTTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPheValIleSerGlu 220
 Db 722 CAACCTTTTGCACAGAGAGCTCTCCAGGCTGTGTAACCTCCCAAGTCAAGAGTGA 781
 QY 221 PheAsnSerTyrSerLeuTrpGlyTyrVal 230
 Db 782 TTCAATTCCTACAGCTGACAGGGATATGTG 811
 RESULT 10
 ABL88167
 ID ABL88167 standard; cDNA; 1475 BP.
 XX ABL88167;
 AC
 DT 16-MAY-2002 (first entry)
 XX
 XX Human PRO1356 cDNA sequence SEQ ID NO:191.
 DE
 XX Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;

KM vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KM angiotensin disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KM age-related macular degeneration; arterial restenosis; angina;
 KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KM wound healing; chromosome mapping; gene mapping; gene; ss.
 XX Homo sapiens.
 XX W0200200690-A2.
 XX 03-JAN-2002.
 XX 20-JUN-2001; 2001WO-US019692.
 XX 23-JUN-2000; 2000US-0213637P.
 XX 20-JUL-2000; 2000US-0219556P.
 XX 25-JUL-2000; 2000US-0220624P.
 XX 25-JUL-2000; 2000US-0220664P.
 XX 28-JUL-2000; 2000WO-US020710.
 XX 02-AUG-2000; 2000US-0222695P.
 XX 17-AUG-2000; 2000US-00643657.
 XX 23-AUG-2000; 2000WO-US023522.
 XX 24-AUG-2000; 2000WO-US023328.
 XX 07-SEP-2000; 2000US-0230978P.
 XX 18-SEP-2000; 2000US-00664610.
 XX 18-SEP-2000; 2000US-00665350.
 XX 24-OCT-2000; 2000US-0242922P.
 XX 08-NOV-2000; 2000US-00709238.
 XX 08-NOV-2000; 2000WO-US030952.
 XX 10-NOV-2000; 2000WO-US030873.
 XX 01-DEC-2000; 2000WO-US032678.
 XX 20-DEC-2000; 2000US-00747259.
 XX 22-JAN-2001; 2001US-00767609.
 XX 28-FEB-2001; 2001US-00796498.
 XX 28-FEB-2001; 2001WO-US006520.
 XX 01-MAR-2001; 2001WO-US006656.
 XX 09-MAR-2001; 2001US-00802706.
 XX 14-MAR-2001; 2001US-00806869.
 XX 22-MAR-2001; 2001US-00816744.
 XX 05-APR-2001; 2001US-00828366.
 XX 10-MAY-2001; 2001US-00854208.
 XX 10-MAY-2001; 2001US-00854280.
 XX 25-MAY-2001; 2001US-00866028.
 XX 25-MAY-2001; 2001US-00866034.
 XX 25-MAY-2001; 2001WO-US017092.
 XX 30-MAY-2001; 2001US-00870574.
 XX 30-MAY-2001; 2001WO-US017443.
 XX 01-JUN-2001; 2001WO-US017800.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Paoi NF, Pi Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoi NF, Pi Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W, WPI; 2002-090516/12.
 XX P-PSDB; ABB84912.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
 XX Claim 2; Fig 191; 565pp; English.
 XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic, antiangiogenic, hypotensive, vulnerable and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, CC proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.

CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration, CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound CC healing. The PRO polynucleotides have applications in molecular biology, CC including use as hybridisation probes, and in chromosome and gene CC mapping. ABL88259 to ABL88267 represent primers and probes used in the CC exemplification of the present invention
 XX
 XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 XX
 XX Alignment Scores:
 XX Pred. No.: 1,51e-122 Length: 1475
 XX Score: 1174.00 Matches: 230
 XX Percent Similarity: 100.00% Conservative: 0
 XX Best Local Similarity: 100.00% Mismatches: 0
 XX Query Match: 100.00% Indels: 0
 XX DB: 6 Gaps: 0
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 XX US-09-787-677a-3 (1-230) x ABL88167 (1-1475)
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 XX QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
 XX Db 122 ATGGCCCTCTTGGCCCTCAACTTGTGGCTACATCTTAAGCCCTTGGGGCTTTTGGC 181
 XX QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValGlyAlaSerIle 40
 XX Db 182 ACACTGGTTCACATGCTGCTCCAGCTGAGAAACAAGTCTTAATGCGGTGCAGCATT 241
 XX QY 41 ValThrAlaValAlaGlyPheSerLeuGlyLeuTyrMetGlyValAlaThrHisSerThrGly 60
 XX Db 242 GTGACAGCACTGCTCTTCCAAAGGCTCTGAGTGAAGTGCACACACAGCAGGCGC 301
 XX QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 XX Db 302 ATCAACCAAGTGTACATCTATACACCCCTCTGGGCTGCGGTGACATCCAGGCTGCC 361
 XX QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 XX Db 362 CAGGCCATGATGTGTGATCATCATCATCTCTCTGCTGCGCATTAATCTGTGTG 421
 XX QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
 XX Db 422 GGCATGATGATGACAGCTTCTGCAAGATCCGAGCCAAACACAGATGGCGTAGCA 481
 XX QY 121 GlyIleValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaIlePheIle 140
 XX Db 482 GGTGAGCTCTTTTCATCTTGAAGGCTCTGGATTCATCTCTGCTGCGAATCTT 541
 XX QY 141 HisGlyIleLeuAlaArgAspPheTyrSerProLeuValProAspSerMetCysPheGlu 160
 XX Db 542 CATGGATCTTCAAGGAGCTTCTACTCACCACTGGTGTGACAGCATGAATTTAGAT 601
 XX QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 XX Db 602 GGAAGGCTCTTATCTTGGCATTAATTTCTCTCTCTCTGATGAGCTGAGATATC 661
 XX QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 XX Db 662 CTCTGCTTTCTGCTCATCTCCAGAGAAATCGCTCAACTACATGAGCTTCAAGGCC 721
 XX QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValAlaValSerGlu 220
 XX Db 722 CAACCTCTTCCCAAGAGAGCTCTCCAAAGGCTGTGTCACCTCCAAAGTCAAGAGTGAG 781
 XX QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 XX Db 782 TTCATTTCTTACAGCCTGACAGAGGATATG 811
 XX
 XX RESULT 11
 XX ABL881089
 XX ID ABL881089 standard; cDNA; 1475 BP.
 XX

ABK11089;
 05-JUN-2002 (first entry)
 CDNA encoding tumour-associated antigenic target protein, TAT134.
 TAT134; Tumour-associated Antigenic Target; tumour; breast cancer;
 colorectal cancer; lung cancer; liver cancer; bladder cancer; melanoma;
 central nervous system cancer; leukemia; gene therapy; gene; ss.
 Homo sapiens.
 Location/Qualifiers
 CDS 122..814
 /tag= a
 /product= "TAT134"
 /note= "Tumour-associated antigenic target"
 WC200216429-A2.
 28-FEB-2002.
 22-JUN-2001; 2001WO-US020118.
 24-AUG-2000; 2000WO-US023328.
 26-SEP-2000; 2000US-0235451P.
 01-DEC-2000; 2000WO-US032678.
 28-FEB-2001; 2001WO-US006520.
 01-MAR-2001; 2001WO-US006666.
 (GETH) GENENTECH INC.
 Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith V,
 Wood WI, Wu TD, Zhang Z;
 WPI; 2002-280917/32.
 P-PSDB; AAU76534.
 Novel isolated tumor-associated antigenic target polypeptides which are
 useful as targets for cancer therapy and diagnosis in mammals.
 Claim 1; Fig 1; 121pp; English.
 The invention relates to an isolated tumour-associated antigenic target
 polypeptide (TAT) (I), specifically TAT134-TAT138 polypeptides, and the
 polynucleotides (II) encoding them. (II) is useful for diagnosing the
 presence of a tumour in a mammal, where the level of expression of (II)
 is indicative of the presence of tumour in the mammal from which the test
 sample was obtained. Antibody to (I) is useful for killing a cancer cell,
 (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell,
 an ovarian cancer cell, a central nervous system (CNS) cancer cell, a
 liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a
 melanoma cell or a leukaemia cell) that expresses (I). Oligonucleotides
 hybridising to (II) are useful as diagnostic probes, antisense
 oligonucleotide probes or for encoding fragments of full length TAT
 polypeptide. (II) is also useful in chromosome and gene mapping and in
 the generation of antisense RNA and DNA probes, for constructing and
 hybridisation probes for mapping the gene encoding TAT and for genetic
 analysis of individuals with genetic disorders. (II) is also useful for
 generating either transgenic animals or knockout animals, and in gene
 therapy. The TAT polypeptides and nucleic acids may also be used for
 tissue typing and the TAT polypeptides are useful for screening compounds
 that mimic the TAT polypeptide (agonist) or prevent the effect of TAT
 polypeptide (antagonist). The antibody is useful for staging TAT
 polypeptide-expressing cancers, purifying or immunoprecipitating TAT
 polypeptide from cells, for detection and quantitation of TAT polypeptide
 in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or
 Western blot. The antibodies are also useful for treating a TAT-
 expressing cancer or alleviating one or more symptoms of cancer in a
 mammal. The present sequence represents the coding sequence of TAT134
 Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1 51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-787-677a-3 (1-230) x ABK11089 (1-1475)
 QY 1 MeelaSerLeuGlyLeuGlnLeuValGlyTYrileuGlyLeuGlyLeuGly 20
 DB 122 ATGGCCTCTTGGGCTCCCAATCTGTGGCTACATCTAGAGCTTGTGGGGCTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLyThrSerSerTYrValGlyAlaSerIle 40
 DB 182 ACCTGGTTCCTAGCTGCTCCCGACGTGAAAACAAGTCTTATGTGCGGTCCAGCATTT 241
 QY 41 ValThrAlaValGlyPheSerLySGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
 DB 242 GTGACAGCAGTTGGCTTCTCCAGGGCTCTGTGATGAAATGTGCCACACAGCAGAGCC 301
 QY 61 IleThrGlnCysAspIleTYrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 DB 302 ATCACCCAGTGTGACATCTATAGACACCTCTGGGCTGCGCTGACATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 362 CAGGCCATGATGGGATCCAGATCCAGCATCTCTCCCTGCGCTGCATTATCTCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaIleYsaAspArgValAlaValAla 120
 DB 422 GGCATGAGATGCACAGCTTCTGTGCCAGATCCGAGCACAAGAGAGCGGTAGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTTPanLeu 140
 DB 482 GGTGAGCTTTTTCATCTGTGAGGCTCTGGGATTCATTCTGTGCTGGAAATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTYrSerProLeuValProAspSerMetLyPheGluIle 160
 DB 542 CATGGATCTTACCGGACTTCTACTCACCTGCTGCTCAAGACATGAATTTGAATTT 601
 QY 161 GlyGlnAlaLeuTYrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 DB 602 GAGAGGCTCTTACTTGGGCATTTCTTCCTGTCTCCGATAGCTGGATCATC 661
 QY 181 LeuCyAspSerCysSerSerGlnArgAsnArgSerAntTYrTYrAspAlaTYrGlnAla 200
 DB 662 CTGTGCTTTTCTGCTCATCCAGAGAAATCGCTCAACTACATCGATGCTTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValIleValSerGly 220
 DB 722 CAACTCTTGGCAAGAGAGCTCTCCAAAGGCTGTCAACCTCCCAAGTCAAGAGTAG 781
 QY 221 PheAsnSerTYrSerLeuThrGlyTYrVal 230
 DB 782 TTCAATTCCTACAGCCCTGACAGGTATGTG 811
 RESULT 12
 ABL95656 standard; cDNA; 1475 BP.
 ID ABL95656
 AC ABL95656;
 XX 19-JUN-2002 (first entry)
 DE Human angiogenesis related cDNA PRO1356 SEQ ID NO: 191.
 XX Human; angiogenesis; PEO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiatic; cyostatic; antiangiogenic; hypotensive; vulnary;
 KW antiarteriosclerotic; gene; ss.

XX Homo sapiens.
 OS
 XX WO200208284-A2.
 PN
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US021735.
 XX
 XX 20-JUL-2000; 2000US-0219556P.
 XX 25-JUL-2000; 2000US-0220624P.
 XX 28-JUL-2000; 2000US-0220664P.
 XX 02-AUG-2000; 2000US-0220710.
 XX 17-AUG-2000; 2000US-0222695P.
 XX 23-AUG-2000; 2000WO-US02352.
 XX 24-AUG-2000; 2000WO-US023328.
 XX 07-SEP-2000; 2000US-0230978P.
 XX 18-SEP-2000; 2000US-00664610.
 XX 24-OCT-2000; 2000US-00665350.
 XX 08-NOV-2000; 2000US-0242922P.
 XX 08-NOV-2000; 2000US-00709238.
 XX 10-NOV-2000; 2000WO-US030873.
 XX 01-DEC-2000; 2000WO-US032678.
 XX 20-DEC-2000; 2000US-00747259.
 XX 20-DEC-2000; 2000WO-US034956.
 XX 22-JAN-2001; 2001US-00767609.
 XX 28-FEB-2001; 2001US-00796498.
 XX 28-FEB-2001; 2001WO-US006520.
 XX 01-MAR-2001; 2001WO-US006666.
 XX 09-MAR-2001; 2001US-00802706.
 XX 14-MAR-2001; 2001US-0080889.
 XX 22-MAR-2001; 2001US-00816744.
 XX 05-APR-2001; 2001US-00828366.
 XX 10-MAY-2001; 2001US-00854208.
 XX 10-MAY-2001; 2001US-00854280.
 XX 25-MAY-2001; 2001US-00866028.
 XX 25-MAY-2001; 2001US-00866034.
 XX 30-MAY-2001; 2001US-00870574.
 XX 30-MAY-2001; 2001WO-US017443.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 20-JUN-2001; 2001WO-US019692.
 XX
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI: 2002-171999/22.
 DR P-PDB: ABB95518.
 XX
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.

PS Claim 1; Fig 191; 567bp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-787-677A-3 (1-230) x ABL95656 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGluValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 Db 122 ATGGCCCTCTTGGCCCTCCCACTTGGGCTGACATCCCTTCTGGGGCTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrThrSerTyrValGlyAlaSerIle 40
 Db 182 ACATGGTTCCTCCATGCTGCTCCCACTGGAAACAGTTCTTATGCGGTGCAGCAT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
 Db 242 GTACACAGAGTTCGCTTCTCCCAAGGCGCTTGATGAAAGTCCACACACACAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrIleLeuGlyLeuProAlaIleGlnAla 80
 Db 302 ATCACCAGGTGATACATCTATACACCTTCTGGGCTGCGCTGCATCCAGCGTGC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 Db 362 CAGGCCATGATGGTGCATCATCGCATCTCTCCCTGGCCCTGATTACTCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAla 120
 Db 422 GGCATGAGATGACACAGCTTCTCCCAAGATCCCGACCAAGACAGAGTGGTAGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrPantLeu 140
 Db 482 GGTGAGTCTTCTTTCATCTTGAAGGCTCTTGGATTCATCTCTGTGCTGGAATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 Db 542 CATGGATCTCTAGGAGACTTCTACTACACCTGCTGCTGACGATGAATTTGAGATT 601
 QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 Db 602 GGAGAGGCTCTTACTTGGGCAATTATTTCTCCCTGTTCTCCCTGATGAGTAATCATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 662 CTCTGCTTTTCTCGCTCATCTCCAGAAATCGCTCAACTACTACATGCTTCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIleValLysSerGlu 220
 Db 722 CAACCTCTTCCCAAGAGAGCTCTCCAGGCCCTGGTCAACCTCCCAAGTCAAGAGTGAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 782 TTCAATTCCTACAGCTGACAGGATATGTG 811
 RESULT 13
 ACA91203

ID ACA91203 standard; cDNA; 1475 BP.
 AC ACA91203;
 DT 11-JUL-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO1356 cDNA.
 KM Human; secreted and transmembrane protein; PRO; antibody therapy;
 KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
 OS Homo sapiens.
 XX
 PN US2003018173-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 01-MAY-2002; 2002US-00063515.
 XX
 PR 06-DEC-2001; 2001US-00006867.
 XX
 PA (GENTH) GENENTECH INC.
 PI Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Matanabe CK, Wood WI;
 XX WPI; 2003-401702/38.
 DR P-PSDB; AB090915.
 XX
 PT New antibody useful for identifying PRO polypeptides, for affinity
 PT purification of PRO polypeptides, and for preparing a medicament for
 PT diagnosing or treating conditions responsive to the antibody or PRO
 PT polypeptide.
 PS Disclosure; Fig 79; 345pp; English.
 XX
 CC The invention describes an antibody that specifically binds to a PRO
 CC polypeptide having a fully defined amino acid sequence given in the
 CC specification. The antibody is useful in identifying PRO polypeptides
 CC useful for various industrial applications, including pharmaceuticals,
 CC diagnostics, biosensors and bioreactors. The antibody is also used for
 CC affinity purification of PRO polypeptides from recombinant cell culture
 CC or natural sources. The antibody, PRO polypeptide, or its agonists or
 CC antagonists, may be used for preparing a medicament for diagnosing or
 CC treating a condition responsive to the antibody, PRO polypeptide, or its
 CC agonists or antagonists. This sequence encodes a novel human secreted and
 CC transmembrane PRO polypeptide
 CC
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
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 Score: 1174.00 Matches: 230
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
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 QY 21 ThrIleuValAlaMetLeuLeuProSerTyrIleThrSerSerTyrValGlyAlaSerIle 40
 Db 182 ACACTGGTTCGACATGCTCTCCAGCTCGAAGAAACAATTCTTATGTCGTCGACGACTT 241
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 Db 242 GTGACACAGCTTGCTTCTCCAAAGGGCTTCGATGTGATGTGCACACAGACAGAGGC 301
 QY 61 IleThrGlnCysAepIleTyrSerThrLeuLeuGlyLeuProAlaAepIleGlnAla 80

Db 302 ATCACCAGGTGACATCTATAGACACCTTCTGGGCTGCGCCGCTGACATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 362 CAGGCCATGATGGTGTGACATCTACATGATGATCTCTCCCTGGCTGCATTAATCTGAGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaValAla 120
 Db 422 GGCATGATGATGACACAGCTTCTTCCAGGATCCGAGCCAAAGACAGAGTGGGGTAGCA 481
 QY 121 GlyIleValIlePhePheIleLeuGlyIleLeuGlyPheIleProValAlaTyrPheLeu 140
 Db 482 GGTGAGATCTTTTCAATCCTTGAGAGGCTCTGGGATTCATTCCTGTCCTGCAATCTT 541
 QY 141 HisGlyIleLeuAlaArgAspPheTyrSerProLeuValProAspSerMetIlePheGluIle 160
 Db 542 CATGGATCTCTACGGGACTTCTACTACACCTGATGTGCAGACATGAATTTGAGATT 601
 QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
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 QY 181 LeuCysePheSerCysSerSerGlnArgAsnArgSerAsnTyrIleAspAlaTyrGlnAla 200
 Db 662 CTCGCTTTTCCGTGCTCATCCAGAAATCGCTCCAACTACATGATGCTTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIleValIleSerGlu 220
 Db 722 CAACCTTTTCCCAAGAGACTCTCCAAAGGCTGTGTCMACTCCCAAGTCMAAGAGTAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 782 TTCAATTCCTACAGCTCGACAGGTATGTG 811
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 ACD81580
 ID ACD81580 standard; cDNA; 1475 BP.
 AC ACD81580;
 DT 18-SEP-2003 (first entry)
 XX
 DE Human cDNA encoding secreted/transmembrane protein PRO1356.
 KM Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;
 KW cytosolic.
 OS Homo sapiens.
 XX
 PN US2003009013-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 01-MAY-2002; 2002US-00063519.
 XX
 PR 30-DEC-1998; 98KR-00062142.
 PR 08-MAR-1999; 99KO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 15-SEP-1999; 99US-00397342.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 30-DEC-1999; 99WO-US031274.
 PR 18-FEB-2000; 2000KO-US004341.
 PR 01-MAR-2000; 2000KO-US005051.
 PR 02-MAR-2000; 2000KO-US005841.
 PR 21-MAR-2000; 2000KO-US007532.
 PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000MO-US015264.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000MO-US030873.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000MO-US034956.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
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 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001MO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-DEC-2001; 2001US-00006867.
 XX (GETH) GENENTECH INC.
 PI Eston DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2003-447384/42.
 DR P-PSDB; ABO33974.
 XX
 PT New isolated antibody specifically binding a PRO polypeptide, useful for
 PT the preparation of a medicament for treating disorders with the aberrant
 PT expression or activity of the PRO polypeptide, such as tumor conditions
 PT and cancer.
 XX
 PS Disclosure; Fig 79; 223pp; English.
 XX
 CC The invention relates to an antibody that binds to a secreted or
 CC transmembrane protein designated PRO146 appearing as ABO33941. The
 CC protein is one of 84 PRO polypeptides which (along with their encoding
 CC nucleic acids) are disclosed in the specification. The methods and
 CC compositions of the present invention are useful for the preparation of a
 CC medicament for the treatment of disorders associated with the aberrant
 CC expression or activity of the PRO polypeptide, such as tumor conditions
 CC and cancer. They can also be used to generate transgenic or knockout
 CC animals useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
 CC molecular weight markers for protein electrophoresis, chromosome
 CC identification and tissue typing. The antibodies may be used in various
 CC diagnostic, competitive binding and/or immunoprecipitation assays. The
 CC present sequence encodes a PRO polypeptide
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 1.51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
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 DB 122 ATGGCCCTCTTGCCCTCAACTGTGGGCTACATCTAGGCCCTTGGGGCTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpIleTherSerSerTyrValGlyAlaSerIle 40
 DB 182 ACACGTGCTGCCATGCTGCTCCACGCTGGAACCAAGTCTTATGTGCGGCGCAGCAT 241
 QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTrpMetGlyCysValATrHisSerThGly 60
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DB 242 GTGACAGCAGTTCCTTCCTCCAGGCGCTCTGATGGAATGTGCCACACAGACAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 DB 302 ATCACCAGGTGATCATCTATACACCTTCCTGGGCTGCCCGCTGACATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValHisSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
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 DB 542 CATGGATCTCTAGGAGACTTCTACTACCACTGTGTCTGACAGCATGAATTTGAGATT 601
 QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 DB 602 GAGAGGCTCTTACTTGGCATATTTCTTCTCTGTTCTCTGATAGCTGGAATATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTrpAspAlaTyrGlnAla 200
 DB 662 CTCGTGCTTTCTCGTCATCATCCAGAAATCGCTCCAACTACTAGATGCTCAAGGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIysValLysSerGlu 220
 DB 722 CAACCTTGTGCCCAAGAGACTCTCCAAAGGCTGTCAACCTCCCAAGTCAAGAGTGA 781
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 RESULT 15
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 AC ACA60402;
 XX
 DT 11-JUN-2003 (first entry)
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 DE Novel human secreted and transmembrane protein PRO1356 cDNA.
 XX
 KW Human; secreted and transmembrane polypeptide; gene;
 KW ss. chromosome mapping; gene mapping; transgenic animal; knockout animal;
 KW therapeutic agent screening; chromosome identification; tissue typing;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003018183-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 01-MAY-2002; 2002US-00063512.
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 PR 06-DEC-2001; 2001US-00006867.
 XX
 XX (GETH) GENENTECH INC.
 PI Eston DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2003-330984/31.
 DR P-PSDB; ABU71991.
 XX
 PT New secreted and transmembrane PRO polypeptides and nucleic acid
 PT molecules encoding the polypeptides, useful in gene therapy or preparing

PT a medicament for treating a condition that is responsive to the PRO polypeptide or antibody.

PS Disclosure; Fig 79; 409pp; English.

XX The invention describes novel isolated PRO polypeptides. The PRO polypeptides or anti-PRO antibodies are useful in preparing a medicament for treating a condition that is responsive to the PRO polypeptide or antibody. The PRO nucleotide sequences may be used as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This sequence encodes a novel human secreted and transmembrane PRO polypeptide

XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1-51e-122	Length:	1475
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
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US-09-787-677A-3 (1-230) x ACA60402 (1-1475)

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Db 182 ACACTGGTGGCAATGCTGCTCCAGCTGGAACCAAGTTCTTATGTCGGTGCAGCATT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGluCysAlaTrpHisSerThrGly 60
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Db 362 CAGGCCATGATGAGATCCAGTCAATCTCCCTCGGCTGCATTATCTGTGGTGG 421
QY 101 GlyMetArgCysTrpValPheCysGlnGlnuSerArgAlaLysAspArgValAlaValAla 120
Db 422 GGCATGAGATGCCACAGCTTCTGCCAGGAATCCGAGCCAAAGACAGATGCCGTAGCA 481
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Db 482 GGTGAGCTTTTTCATCTCTTGAGGCTCTCTGGGATTCATTCTGTGCTGGAATCTT 541
QY 141 HisGlyIleLeuAlaGaaPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 542 CATGGATCTCTACCGGACTTCTACTCACCTGATGCTGACACATGAAATTTGAGATT 601
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Db 602 GGAGAGGCTCTTTTACTTGGGCAATTTCTTCTCTCTGATGCTGGAATCATC 661
QY 181 LeuCyAsPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCTCTCTCTCCAGGAAATCGTCCAACTACTAGATGCTTACCAAGCC 721

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QY 201 GluProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db 722 CAACCTTCTCCACAGGAGCTCTCCAGGCTGTGTCACCTCCAAAGTCAGAGTGAAG 781

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QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
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Search completed: December 20, 2004, 14:45:07
Job time : 504 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 14:29:01 ; Search time 93 Seconds
(without alignments)
1757.865 Million cell updates/sec

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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1174	100.0	1400	US-09-663-600A-139	Sequence 139, App
2	1174	100.0	1475	US-10-140-002-491	Sequence 491, App
3	1162	99.0	1524	US-09-663-600A-45	Sequence 45, App1
4	442.5	37.7	1665	US-09-300-958A-22	Sequence 22, App1
5	442.5	37.7	1705	US-09-205-258-106	Sequence 106, App
6	437	37.2	708	US-09-620-312D-986	Sequence 986, App
7	430	36.6	1253	US-09-673-395A-71	Sequence 71, App1
8	422	35.9	1554	US-09-895-652A-14	Sequence 14, App1
9	407.5	34.7	3443	US-09-886-683A-3	Sequence 3, App1
10	407.5	34.7	3483	US-09-130-491-3	Sequence 3, App1
11	380	32.4	1722	US-09-489-847-93	Sequence 93, App1
12	334	28.4	1380	US-09-489-847-125	Sequence 125, App

13	314.5	26.8	1155	4	US-09-603-552-2	Sequence 2, App1
14	275	23.4	1353	3	US-09-724-864-32	Sequence 32, App1
15	232	19.8	363	2	US-08-966-316-8	Sequence 8, App1
16	229	19.5	413	3	US-09-188-930-55	Sequence 55, App1
17	229	19.5	413	4	US-09-312-283C-55	Sequence 55, App
18	225.5	19.2	615	4	US-09-621-976-1835	Sequence 1835, App
19	221	18.8	441	4	US-09-404-879A-104	Sequence 104, App
20	221	18.8	441	4	US-09-338-933-104	Sequence 104, App
21	221	18.8	441	4	US-09-215-681-104	Sequence 104, App
22	221	18.8	441	4	US-09-216-003A-104	Sequence 104, App
23	221	18.8	441	4	US-09-667-857-104	Sequence 104, App
24	198	16.9	427	4	US-09-603-552-8	Sequence 8, App1
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29	174.5	14.9	413	4	US-09-621-976-360	Sequence 360, App
30	161.5	13.8	541	4	US-09-603-552-7	Sequence 7, App1
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33	126	10.7	208	4	US-09-603-552-10	Sequence 10, App1
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35	124.5	10.6	316	4	US-09-736-457-976	Sequence 976, App
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37	124.5	10.6	316	4	US-09-671-325-976	Sequence 976, App
38	124.5	10.6	316	4	US-09-658-824-976	Sequence 976, App
39	119.5	10.2	1558	3	US-09-123-030-7	Sequence 7, App1
40	106.5	9.1	350	4	US-09-621-976-13474	Sequence 13474, A
41	100	8.5	1332	4	US-09-489-039A-995	Sequence 995, App
42	99	8.4	840	4	US-09-252-991A-14392	Sequence 14392, A
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45	98	8.3	89047	4	US-09-596-002-34	Sequence 34, App1

ALIGNMENTS

RESULT 1
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Sequence 139, App
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducleret, Aymric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig.peptide
LOCATION: 36..107
OTHER INFORMATION: Von Heijne matrix

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US-09-663-600A-139

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Query Match: 100.00% Indels: 0
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Db 216 ATCAACCCAGTGTGACATCTATAGACCCCTTGGGCTGCCGCTGACATCCAGGCTGCC 275
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Db 276 CAGGCCATGATGTGAGATCCAGATCCAGATCTCCCTGCGCTCATTAATCTGTGTG 335
Qy 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
Db 336 GGCATGAGATGACAGATCTTCTGACAGAAATCCGAGCCAAAGACAGATGGCGGTAGCA 395
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrAsnLeu 140
Db 396 GGTGGATCTTTTTCATCTTGGAGGCTCTCGGATTCATCTCTGTGCTGGAATCTT 455
Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 456 CATGGATCTTACCGGAGCTTCTACTCACACTGGTGCCTGACAGCATGAATTTGAAGATT 515
Qy 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 516 GGAAGAGCTCTTAACTGGGATTAATTTCTCTCCCTGATTCCTCGAATGCAATATATC 575
Qy 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 576 CTCTGCTTTTCTGCTCATCTCCAGAAATAGCTTCAACTACTGATGCTTCAACAGCC 635
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
Db 636 CAACCTCTTCCACAGAGAGCTCTCCAAAGGCTGGTCAACCTCCCAAGTCAAGAGAGAG 695
Qy 221 PheAsnSerTyrSerLeuThgIyTyrVal 230
Db 696 TTCATATCTTACACGCTGACAGGGGTATGTG 725

RESULT 2
US-10-140-002-491
; Sequence 491. Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```

```
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Inc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 491
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-002-491

Alignment Scores:
Pred. No.: 3.64e-142 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-787-677A-3 (1-230) x US-10-140-002-491 (1-1475)
Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 122 ATGGCCCTCTTGGCCCTCCAACTTGCGGCTACATCTAGGCCCTTGGGGCTTTGGGC 181
Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
Db 182 ACACGTGCTGCATGCTGCTCCAGCTGGAACAAAGTTCTATGTCGGTGCAGCATT 241
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThgIy 60
Db 242 GTGACAGCAGTGTGCTTCTCCAGAGGCTCTGAGTGAATGTGCACACACAGCAGGC 301
Qy 61 IleThrGlnCysAAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCAACCCAGTGTGACATCTATAGACCCCTTGGGCTGCCGCTGACATCCAGGCTGCC 361
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 362 CAGGCCATGATGTGAGATCCAGATGCAATCTCTCCCTGCGCTGATTAATCTGTGTG 421
Qy 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
Db 422 GGCATGAGATGACAGATCTTCTCCAGAAATCCGAGCCAAAGACAGATGGCGGTAGCA 481
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrAsnLeu 140
Db 482 GGTGGATCTTTTTCATCTTGGAGGCTCTCGGATTCATCTCTGTGCTGGAATCTT 541
Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 542 CATGGATCTTACCGGAGCTTCTACTCACACTGGTGCCTGACAGCATGAATTTGAAGATT 601
Qy 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAAGAGCTCTTAACTGGGATTAATTTCTCTCCCTGATTCCTCGAATGCAATATATC 661
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QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
DB 662 CTCCTGCTTTCCGCTCATCTCCAGAGAAATCGCTCCAACTACACATGCTCTCCAGGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlyValLysSerGlu 220
DB 722 CAACCTCTTGCCCAAGAGAGCTCTCCAGAGCGCTGGTCAACCTCCCAAGTCAAGAGTGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCATTCTACAGCGCTGACAGGGTATGTC 811
RESULT 3
US-09-663-600A-45
Sequence 45, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducleit, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 45
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 160..231
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.6999980926514
NAME/KEY: polyA_signal
LOCATION: 1510..1515
NAME/KEY: polyA_site
LOCATION: 1506..1519
NAME/KEY: misc_feature
LOCATION: 1048..1504
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA552647
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 597..846
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA345449
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 39..53
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA345449
NAME/KEY: misc_feature
LOCATION: 113..149
OTHER INFORMATION: homology

OTHER INFORMATION: id: AA345449
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 98..400
OTHER INFORMATION: homology
OTHER INFORMATION: id: T86266
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 1210..1489
OTHER INFORMATION: homology
OTHER INFORMATION: id: T86158
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 954..983
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA16709
OTHER INFORMATION: est
US-09-663-600A-45
Alignment Scores:
Pred. No.: 1,39e-140 Length: 1524
Score: 1162.00 Matches: 228
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 2
Query Match: 98.98% Indels: 0
DB: 4 Gaps: 0
US-09-787-677A-3 (1-230) x US-09-663-600A-45 (1-1524)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
DB 160 ATGGCTCTTGCTGGCTTCCCACTTGTGGCTACATCTAGCGCTTCTGGGGCTTTGGGC 219
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
DB 220 ACAGCTGTGCCATGCTGCTCCCACTGGAAGAAACAAGTTCTTATGCGGTGCAGCAT 279
QY 41 ValThrAlaValGlyPheSerTyrGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
DB 280 GTGACAGAGTGGCTTCTCCCAAGGGCTCTGTGATGGAATGTCCACACACACAGCGC 339
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
DB 340 ATCACCAGGTGACATCTATAGCACCTTGTGGCTGCGCTGACATCCAKGCTGCC 399
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 400 CAGGCCATATGCTGATCATCTACATGCAATCTCTCCCTGGCGCATTAATCTGTGGTG 459
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaVal 120
DB 460 GGCATGATATGACACAGTCTTCTCCAGGAATCCCGAGCCAAAGACAGAGTGGCGTAGCA 519
QY 121 GlyValValPheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrPheLeu 140
DB 520 GTTGGAGTCTTTTCATCTTGGAGGCTCTGGAATCAATCTCTGTGCTGGAATCT 579
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlu 160
DB 580 CATGGATCTTACGGAGACTTCTACTCAGCATGCTGCTCAGCATGAATTTGAGATT 639
QY 161 GlyValAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
DB 640 GGAGAGGCTCTTACCTGGGCAATTAATTTCTCTCCCTGTGATGAGTGAATCATC 699
QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
DB 700 CTCCTGCTTTCCGCTCATCTCCAGAGAAATCGCTCCAACTACACATGCTCTCCAGGCC 759
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlyValLysSerGlu 220
DB 760 CAACCTCTTGCCCAAGAGAGCTCTCCAGAGCGCTGGTCAACCTCCCAAGTCAAGAGTGAG 819

Qy 221 PhenanserYrSerLeuThnGlyTyVal 230
Db 820 TTCATTCTTACAGCTGACGAGGTATGTG 849

RESULT 4
US-09-300-958A-22
Sequence 22, Application US/09300958A
Patent No. 6495319
GENERAL INFORMATION:
APPLICANT: McCelland, Michael
APPLICANT: Welsh, John
APPLICANT: Trenkle, Thomas
TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
TITLE OF INVENTION: Using Same
FILE REFERENCE: P-PH 3457
CURRENT APPLICATION NUMBER: US/09/300,958A
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/083,331
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/098,070
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: 60/118,624
PRIOR FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 1665
TYPE: DNA
ORGANISM: Homo sapiens
US-09-300-958A-22

Alignment Scores:
Pred. No.: 4,34e-47 Length: 1665
Score: 442.50 Matches: 82
Percent Similarity: 63.94% Conservative: 51
Best Local Similarity: 39.42% Mismatches: 70
Query Match: 37.69% Indels: 5
Gaps: 1

US-09-787-677a-3 (1-230) x US-09-300-958A-22 (1-1665)

Qy 1 MethlaSerLeuGlyLeuGlnLeuValGlyTyrlleLeuGlyLeuGlyLeuGly 20
Db 183 ATGGCCCTCCATGGGGCTACAGGTATGGGATCCGGCTGCGCTGGGCTGGCTGCC 242

Qy 21 ThrleuValAlaMetLeuLeuProSerTrpLysTrpSerSerTyValGlyAlaSerlle 40
Db 243 GTCATGCTGCTGCTGGCGGCTGCCATGTGGCGCGTGAACGCTTCATCGGACAGCAATT 302

Qy 41 ValThrAlaValGlyPheSerTrpLeuGlyLeuTrpMetGlyCysAlaThrHleSerThnGly 60
Db 303 GTCACCTCGCAGACCATCTGGAGGGCTTATGATGAACCTGCGGTGCAGACGACGCC 362

Qy 61 IleThnGlnCysAspIleTyTrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 363 CAGATGACAGTCAAGGTGATGACGCTGCTGACACTGGCGGACGAGACTGACGCGGCC 422

Qy 81 GlnAlaMetMetValIleTrSerSerAlaIleSerSerLeuAlaCysIlelleSerValVal 100
Db 423 CGCCCTCGTCATCATCATCATCATCTGCTGCTGCGGCGTGGCTGCTGCTGCTGCTG 482

Qy 101 GlnMetTrpCysTrpValPheCysGlnGlnSerAlaValAspArgValAlaValAla 120
Db 483 GGGGGCAGGTATCAACATGCTGAGAGATGAAGCGCAAGCGCAAGACCATATGATGTG 542

Qy 121 GlnGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
Db 543 GCGGGCGGTGCTTCTGTTGGCGGCTTATGTGATGATGACGCGGTGCTTCTGACGCC 602

Qy 141 HisGlyIleLeuAlaGlnPheTyTrSerProLeuValProAspSerMetLysPheGluIle 160
Db 603 CACAACATCATCAAGACTTCTACATCCGCTGCTGCTGCTGCTGCTGCGGACGAGAGATG 662

Qy 161 GlnAlaLeuTyTrleuGlyIlelleSerSerLeuPheSerLeuIleAlaGlyIlelle 180
Db 663 GGGGCTCGCTTACATCGCTGAGCGGCTCGGCTGCTGCTGCTGCTGCGGGGAGCTG 722

Qy 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyTrValAlaTyGlnAla 200
Db 723 CTTTGGCTGCAACGTCTCACCCCGCACAGACAGCAGCAGCAGCAGCAGCAGCAGCAGC 767

Qy 201 GlnProLeuAlaThrArgSerSer 208
Db 768 AAGATTCTCTGCGGCTGCTGCT 791

RESULT 5
US-09-205-258-106
Sequence 106, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: PCT/US98/11422
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/048,885
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,375
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,881
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,880
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,896
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,020
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,876
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,895
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,884
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,894
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,971
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,882
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,899
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,893
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,900
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,901
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,892
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,915
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,019
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,972
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,916
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,373
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,875

EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049,374
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,917
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,949
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,974
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,883
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,897
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,898
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,962
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,963
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,877
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,878
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/070,923
 EARLIER FILING DATE: 1997-12-18
 EARLIER APPLICATION NUMBER: 60/092,921
 EARLIER FILING DATE: 1998-07-15
 EARLIER APPLICATION NUMBER: 60/094,657
 EARLIER FILING DATE: 1998-07-30
 NUMBER OF SEQ ID NOS: 1227
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 106
 LENGTH: 1705
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (724)
 OTHER INFORMATION: n equals a,t,g, or c
 US-09-205-258-106

Alignment Scores:

Pred. No.: 4,52e-47 Length: 1705
 Score: 442.50 Matches: 82
 Percent Similarity: 63.94% Conservative: 51
 Best Local Similarity: 39.42% Mismatches: 70
 Query Match: 37.69% Indels: 5
 DB: 4 Gaps: 1

US-09-787-677A-3 (1-230) x US-09-205-258-106 (1-1705)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly
 DB 209 ATGGCCCTCCATGGGGGACAGGTATAGGCGATGGCGGCGTCCCTGGCTGGCGCC 268
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrrPlyThrSerSerTrrValGlyAlaSerIle 40
 DB 269 GTCATGCTGTGCTGGCGGCTGCCCATGTGGCGGCTGACGCGCTTCATCGGACGACATT 328
 QY 41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrrMetGlyCysAlaIleThrIleSerThrGly 60
 DB 329 GTACCTCCGACGACATCTGGAGGAGGCTTATGATGAATGCGGTGGCGACAGCGCGCC 388
 QY 61 IleThrGlnCysAspIleTrrSerThrLeuGlyLeuProAlaAspIleGlnAlaIle 80
 DB 389 CAGATGACGTGCAAGGTGTAAGACTGCTGCTGACATGGCGGACGACGCGCGCC 448
 QY 81 GlnAlaMetMetValTrrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 449 CGGCGCTCTGCTATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 508
 QY 101 GlnMetArgCysThrValAlaPheCysGlnGluSerArgAlaIleValAspArgValAlaValAla 120

DB 509 GGGGCAAGTGTACCAACTGCTGGAGGATGAAGCGCCCAAGCGCAACCATGATCTGTG 568
 QY 121 GlyGlyValPhePheIleLeuGlyLeuGlyPheIleProValAlaTrrPheLeu 140
 DB 569 GCGGCGGTGTGTTCTGCTGGCGGCTTATGTGATGATGCGGCTGCTGCGGCGCC 628
 QY 141 HisGlyIleLeuArgAspPheTrrSerProLeuValProAspSerMetLysPheGlnIle 160
 DB 629 CACAACATCATCCAAAGCTTCTACATCCGCTGTGGCTCCGGGCGAAGCGGAGATG 688
 QY 161 GlyIleAlaLeuTrrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 DB 689 GGTGCTGCTGTACGTCGCTGGCGGCTCCGAGTGTCTGCTCTTGGCGGCGGCTG 748
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTrrTrrAspAlaTrrGlnAla 200
 DB 749 CTTGTGCAACTGTTCACCCCGACAGCAAG-----CCTTACTCGGCC 793
 QY 201 GlnProLeuAlaThrArgSerSer 208
 DB 794 AAGTATTCGTGCTGCCGCTGTGCT 817

RESULT 6

US-09-620-312D-986
 Patent No. 659662
 GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Asundi, Vinod
 APPLICANT: Zhang, Jie
 APPLICANT: Ren, Feiyan
 APPLICANT: Chen, Rui-hong
 APPLICANT: Zhao, Qing A.
 APPLICANT: Wehrman, Tom
 APPLICANT: Xue, Aidong J.
 APPLICANT: Yang, Yonghong
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Ma, Yungqing
 APPLICANT: Wang, Dunrui
 APPLICANT: Wang, Zhiwei
 APPLICANT: John Tillinghast
 APPLICANT: Drmanac, Radoje T.
 TITLE OF INVENTION: No. 659662e1 Nucleic Acids and
 FILE REFERENCE: 784CIP28
 CURRENT APPLICATION NUMBER: US/09/620,312D
 CURRENT FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: 09/552,317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1105
 SOFTWARE: PC_FL_genes Version 1.0
 SEQ ID NO 986
 LENGTH: 708
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (46)..(708)
 US-09-620-312D-986

Alignment Scores:

Pred. No.: 5.54e-47 Length: 708
 Score: 437.00 Matches: 83
 Percent Similarity: 60.19% Conservative: 44
 Best Local Similarity: 39.34% Mismatches: 82
 Query Match: 37.22% Indels: 2
 DB: 4 Gaps: 1

US-09-787-677A-3 (1-230) x US-09-620-312D-986 (1-708)

[illegible]

Query Match:	36.63%	Indels:	13
DB:	4	Gaps:	4
US-09-787-677A-3 (1-230) x US-09-673-395A-71 (1-1253)			
QY	1 MetalaserLeuGlnLeuValGlyTyrileLeuGlyLeuLeuGlyLeuGly 20		
DB	346 ATGGCAATTCGGGCGCTGCACTTGGCTTCTCCATGAGCCCTGCTGGCTGGGTGCT 405		
QY	21 ThrLeuValAlaMetLeuLeuProSerTprlysrhSerSerTyrValGlyAlaSerile 40		
DB	406 CTGGTGGCGCTGCACCGCCATCCCGAGTGGCAGATGAGCTCTCATCGGGTGACATC 465		
QY	41 ValThrAlaValGlyPheSerTyrGlyLeuTprMetGluCValaLthrHsserrngly 60		
DB	466 ATCAGCGCCCGACCGCATGATACAGGGCGTGGATGAGCTGCTCAGCAGACACGGGG 525		
QY	61 IethrGlnCyAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80		
DB	526 ATGATGAGCTGCMAAATGATACACACTGGCTCTCGCTTCCGGCGCCCTGACGGCCACT 585		
QY	81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100		
DB	586 CGAGCGCTAATGTGTGTCTCCTCGTGGTGGGCTTCTGGCCATGTGTTGGGCCAGATG 645		
QY	101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAsp--ArgValAlaVal 119		
DB	646 GGCATGAAAGTGCACCGCTGTGGGGAGACGACMAAGTAGAAGAGCCGATATAGCATG 705		
QY	120 AlaGlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTprAsn 139		
DB	706 GGTGAGGACATATTTTCTCATCTGGGACAGTCTTCCGCTTGTGTACTGCTCTGTAT 765		
QY	140 LeuHISgIyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlu 159		
DB	766 GGCATCAGATGTGTACAGACTTTTATATACCTTTGATCCCTACCAACTTAAAGTATGAG 825		
QY	160 IlegIyGluAlaLeuTyrIleuGlyIleIleSerSerLeuPheSerIleuIleAlaGlyIle 179		
DB	826 TTTGGCCCTGCATCTTATATGCTGGGCGAGGCTGCCCTAGTCACTCTGGAGGTGCA 885		
QY	180 IleLeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGln 199		
DB	886 CTGCTCTCTCTTCTTCTGTCTGTGGATGAGACAGCGCTGGTAC----- 930		
QY	200 AlaGlnProLeuAlaThrArgSerSerProArg-ProGlyGlnProProLysValLysSe 219		
DB	931 -----CGTGCACCCCGCTCTTACCTTAAGTCA---ACTCTTCMAAGAGTATGTG 978		
QY	219 rGluPheAsnSer-----TyrSerIleuThrGlyTyr 229		
DB	979 TGACCTGGGATCTCTTGGCCCGACGCTGACAGGCTAT 1015		
RESULT 8			
US-09-895-652A-14			
/ Sequence 14, Application US/09895652A			
/ Patent No. 6774223			
/ GENERAL INFORMATION:			
/ APPLICANT: Macina, Roberta			
/ APPLICANT: Pillai, Rageswari			
/ TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and			
/ FILE REFERENCE: DEX-0211			
/ CURRENT APPLICATION NUMBER: US/09/895,652A			
/ CURRENT FILING DATE: 2001-06-28			
/ PRIOR APPLICATION NUMBER: 60/214,515			
/ PRIOR FILING DATE: 2000-06-28			
/ NUMBER OF SEQ ID NOS: 39			
/ SOFTWARE: PatentIn Ver. 2.1			
/ SEQ ID NO 14			
/ LENGTH: 1554			
/ TYPE: DNA			
/ ORGANISM: Homo sapiens			

```

FEATURE:
NAME/KEY: unsure
LOCATION: (1544)
US-09-895-652A-14

Alignment Scores:
Pred. No.: 1,78e-44 Length: 1554
Score: 422.00 Matches: 89
Percent Similarity: 57.94% Conservative: 46
Best Local Similarity: 38.20% Mismatches: 86
Query Match: 35.95% Indels: 12
DB: 4 Gaps: 3

US-09-787-677A-3 (1-230) x US-09-895-652A-14 (1-1554)
QY 1 MetAlaserleuGlyleuGlnleuValGlyTyrIleleuGlyLeuLeuGlyleuGly 20
DB 434 ATGGCCAAATTCGGGCTCGAGTGTGGCTTCCATGGGCTGCTGGGCTGGGCTGGG 493
QY 20 YHrleuValAlaMetleuLeuProSerTrrpLyThrSerTyrValGlyAlaSerI 40
DB 494 TCTGGTGGCTGGACCGCCATCCCGCAGTGCAGATGCTCCATGCGGGTGCACAT 553
QY 40 eValTrrAlaValGlyPheSerlysglyLeuTrrpMetGluCysAlaThrHisSerThr 60
DB 554 CATCAGCGCCAGCCCATGTACAGGGGCTGTGGATGACTGCTCCAGCAGACAGCGG 613
QY 60 YIleThrGlnCysAspIleTyrSerThrleuLeuGlyLeuProAlaAspIleGlnAla 80
DB 614 GATGATGAGTGGCAAAATGTACACTGCTGCTGCCCTTCCCGGCTTCAGAGCCAC 673
QY 80 aglnAlaMetMetValThrSerSerAlaIleSerSerleuAlaCysIleIleSerVal 100
DB 674 TCCAGCCCTAATGTGTGCTCTCCCTGCTGCGGCTTCTCCATTTGTGGCCAGAT 733
QY 100 lGlyMetArgCysThrValPheCysGlnGlnuserArgAlaLysAsp---ArgValAla 119
DB 734 GGGCATGAAGTGCAGCGGCTGTGGGGGAGACAGAACAAAGTGAAGAGCCGATAGCAT 793
QY 119 lAlaGlyGlyValPhePheIleleuGlyGlyLeuLeuGlyPheIleProValAlaTrpAs 139
DB 794 GGGTGAAGGATATTTTATCTGTGGCAGGCTTGGCCCTTGGTACTTGTCTCTGTA 853
QY 139 nLeuHISGlyIleLeuArgAspPheTyrSerProleuValProAspSerMetLysPheG 159
DB 854 TGGCATTCAGATTTGTACAGACTTTTATACCTTTGATCCCTTACCAACTTAAGTATGA 913
QY 159 uIleGlyGlyAlaLeuTyrleuGlyIleIleSerSerleuPheSerleuIleAlaGly 179
DB 914 GTTGGCCCTGCATCTTATATGTGCTGGGCAAGGCTGCTCCCTAATCTCTGGAGGTGC 973
QY 179 eIleLeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyr---TyrAspAla 198
DB 974 ACTGCTCTCTGTTCCGTCTCGTCTGGGATGAGAGCAGAGCGGTGATACCCGCTC 1033
QY 198 YrGlnAlaGlnProleuAlaThrArgSerSerProArgProGlyGlnProProLysVal 218
DB 1034 TTACCCCTAAGTCCAACTCTTCAAGGAGTATGTGTGACTGGGATCTCCT----- 1083
QY 218 YsSerGlnPheAsnSerTyrSerleuThrGlyTyr 229
DB 1084 -----TGCCTCAGCTGCAGAGCTAT 1104

RESULT 9
US-09-886-683A-3
Sequence 3, Application US/09886683A
Patent No. 6627439
GENERAL INFORMATION:
APPLICANT: Hoevel, Thorsten
APPLICANT: Koch, Stefan
APPLICANT: Kuchies, Manfred
APPLICANT: Mundigl, Olaf
APPLICANT: Rueger, Petra

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TITLE OF INVENTION: Antibodies against SEMP1 (p23)
FILE REFERENCE: Case 20692
CURRENT APPLICATION NUMBER: US/09/886, 683A
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: EP00113344.6
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: EP01107799.7
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 3443
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (221) .. (853)
US-09-886-683A-3

Alignment Scores:
Pred. No.: 5.01e-42 Length: 3443
Score: 407.50 Matches: 81
Percent Similarity: 56.22% Conservative: 41
Best Local Similarity: 37.33% Mismatches: 78
Query Match: 34.71% Indels: 17
DB: 4 Gaps: 2

US-09-787-677A-3 (1-230) x US-09-886-683A-3 (1-3443)
QY 1 MetAlaserleuGlyleuGlnleuValGlyTyrIleleuGlyleuLeuGlyleuGly 20
DB 221 ATGGCCAAATTCGGGCTCGAGTGTGGCTTCCATTTCCCTTCCGGATGATCGG 280
QY 21 ThleuValAlaMetleuLeuProSerTrrpLyThrSerSerTyrValGlyAlaSerIle 40
DB 281 GCGATGTGACGACCTGCCCTGCCAGTGGAGATTTACTTCATGCGCGGCGAACATC 340
QY 41 ValThrAlaValGlyPheSerlysglyLeuTrrpMetGluCysAlaThrHisSerThr 60
DB 341 GTGACCGCCAGCCCATGTACAGGGGCTGTGGATGCTCCGCTGTGCGCAGACACCGG 400
QY 61 lIleThrGlnCysAspIleTyrSerThrleuLeuGlyLeuProAlaAspIleGlnAla 80
DB 401 CAGATTCAGTGCAGAACTTTGACTCTTCTGCTAATCTGACAGCATTGCAAGCAACC 460
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerleuAlaCysIleIleSerVal 100
DB 461 CCGCTTGAATGCTGTGGTGTGSCATCTCCTGGAGTGAATGACATCTTGTGGCACCGTT 520
QY 101 GlyMetArgCysThrValPheCysGlnGlnuserArgAla---LysAspArgValAlaVal 119
DB 521 GGCATGAAGTGTGAAGTCTTGGAAAGCATGAGGTGCAGAAAGATGAGAGGCTGTC 580
QY 120 AlAGlyGlyValPhePheIleleuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsn 139
DB 581 ATGGGGGCTCGATATTTCTTTCGACGCTGCTGCTATTTTATGTGCGACAGATGGTAT 640
QY 140 LeuHISGlyIleLeuArgAspPheTyrSerProleuValProAspSerMetLysPheG 159
DB 641 GGCATGAAGATCTTCAAGATTTCTATGACCTTATGACCCATGCAATGCAGAGTGA 700
QY 160 lIleGlyGlyAlaLeuTyrleuGlyIleIleSerSerleuPheSerleuIleAlaGly 179
DB 701 TTTGGTCAAGGCTCTTCACTGCTGGGCTGCTGCTTCTCTGCTTGGAGGTGCC 760
QY 180 lIleLeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGln 199
DB 761 CTACTTGTCTGTCTCT----- 778
QY 200 AlAGlnProleuAlaThrArgSerSerProArgProGlyGlnProProLys 216
DB 779 -----CCCCGAAACCAACTCTTACCCACACAGAGCCCATCCAAA 823

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RESULT 10
US-09-130-491-3
/ Sequence 3, Application US/09130491
/ Patent No. 6416974
/ GENERAL INFORMATION:
/ APPLICANT: Holtzman, Douglas A.
/ APPLICANT: Goodheart, Andrew D.J.
/ TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
/ FILE REFERENCE: 09404/041001
/ CURRENT APPLICATION NUMBER: US/09/130,491
/ EARLIER FILING DATE: 1998-08-07
/ EARLIER APPLICATION NUMBER: US 60/058,108
/ EARLIER FILING DATE: 1997-09-05
/ EARLIER APPLICATION NUMBER: US 60/054,961
/ EARLIER FILING DATE: 1997-08-06
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 3483
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (240)...(872)
US-09-130-491-3

Alignment Scores:
Pred. No.: 5,1e-42 Length: 3483
Score: 407.50 Matches: 81
Percent Similarity: 56.22% Conservative: 41
Best Local Similarity: 37.33% Mismatches: 78
Query Match: 34.71% Indels: 17
DB: Gaps: 2

US-09-787-677a-3 (1-230) x US-09-130-491-3 (1-3483)
Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly 20
Db 240 ATGGCCCAACCGCGGCGGCTGCGAGCTTGGGCTTCTTCGCGCTTCCGCGGATGATGCGC 299
Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpIleThrSerSerTrpValGlyAlaSerIle 40
Db 300 GCATCGTCGACGACTGCGCCGCCAGTGAGATTACTCTTATGCGCGGACACATC 359
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 360 GTGACCCGCCAGCGCATGTACGAGGCGCTGTGATGTCCTGCGTGCAGACACCGCG 419
Qy 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
Db 420 CAGATCCAGTGCAGAAAGCTTGTGACTCTTGTGATCTGACGACACATTCAGACCA 479
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 480 CGTGCCCTGATGGTGGTGGCATCTCTCGGAGTAGCATCTTGTGCGACCGTT 539
Qy 101 GlyMetArgCysThrValPheCysGlnGluSerArgAla---IysAspArgValAlaVal 119
Db 540 GGCATGAGGTATGAAGTGGCTTGAAGACGATGAGGTGAGGATGAGATGAGATGCT 599
Qy 120 AlaGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsn 139
Db 600 ATGGGGGTGCGAATTTCTTCTTGCAGGTGCTGCTATTTAGTTGCCACAGCATGGTAT 659
Qy 140 LeuHisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLeuPheGlu 159
Db 660 GGCATAGATGATCTTCAAGATCTTATGACCTTATGACCCAGTCATGACGAGTACGAA 719
Qy 160 IleGlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 179
Db 720 TTGGTAGGCTCTTCTTCACTGCTGAGGCTGCTCTTCTCTCTGCTTGGGAGGCTGCC 779
Qy 180 IleLeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGln 199

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Db 780 CTACTTGTCTGCTCTGCT----- 797
Qy 200 AlaGlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolys 216
Db 798 -----CCCCGAAAAACACTCTTACCCACCAAGGCCCTATCCAAAA 842

RESULT 11
US-09-489-847-93
/ Sequence 93, Application US/09489847
/ Patent No. 6476195
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al
/ TITLE OF INVENTION: 98 Human Secreted Proteins
/ FILE REFERENCE: P2031P1
/ CURRENT APPLICATION NUMBER: US/09/489,847
/ EARLIER FILING DATE: 2000-01-24
/ EARLIER APPLICATION NUMBER: PCT/US99/17130
/ EARLIER FILING DATE: 1999-07-29
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ EARLIER APPLICATION NUMBER: 60/095,486
/ EARLIER FILING DATE: 1998-08-05
/ EARLIER APPLICATION NUMBER: 60/096,319
/ EARLIER FILING DATE: 1998-08-12
/ EARLIER APPLICATION NUMBER: 60/095,454
/ EARLIER FILING DATE: 1998-08-06
/ EARLIER APPLICATION NUMBER: 60/095,455
/ NUMBER OF SEQ ID NOS: 1998-08-06
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 93
/ LENGTH: 1722
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-489-847-93

Alignment Scores:
Pred. No.: 6e-39 Length: 1722
Score: 380.00 Matches: 79
Percent Similarity: 57.45% Conservative: 56
Best Local Similarity: 33.62% Mismatches: 82
Query Match: 32.37% Indels: 18
DB: Gaps: 4

US-09-787-677a-3 (1-230) x US-09-489-847-93 (1-1722)
Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly 20
Db 461 ATGGGGTCCCGACGGGTGAGATCTGCGGCTGTGCTGTGCTGTGCGGCTGGGGGT 520
Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpIleThrSerSerTrpValGlyAlaSerIle 40
Db 521 CTGATCTGCGCGCGGCGGCCCATGTGACAGTGCACCGCTTCTCGACCAACATC 580
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 581 GTGACCGCGACGACCACTGTGAAGGCGCTGTGATGTCGTCGTCGTCGACAGACGCGG 640
Qy 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
Db 641 CACATGACGTGCAAGATGTACGACTGCTGCTGCTGTGACACCGAGTGCAGGCGCG 700
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 701 CGGCGCTGACCGCGGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCG 760
Qy 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIysAspArgValAlaValAla 120
Db 761 GGGCGCGAGTGCACACCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCAG 820
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140

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QY 23 ValAlaMetLeuProSer-----TrpIleThrSerSerTyValAlaSerIle 40
DB 379 CTGGGGGTGACTCGCCAAACGACTACTGCGAGTGTCCACT---GGACCGGAGAGCTC 435
QY 41 ValThrAlaValGlyPheSerTyGlyLeuTrpMetGluCysAlaThrHisSerThyl 60
DB 436 ATCAACCAACCAACCACTTCCGAGAACCTCTGCTTACCTGTGACCTGACCTCCCTGGC 495
QY 61 IleThrGlnCysAspIleTySerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
DB 496 GTCTACAACTGCTGGAGTTCCTCCCTCATGCTGCGCTCTGCGGTATATTCAGGCTGC 555
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 556 CGGCGACTCATGATGACCGCCATCTCTCGGCTTCTCGGCTCTTGGCATGCGATCGC 615
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaVal 120
DB 616 GGCCTGCTGCTGCAACCACTT-----GGGCGCTGAGAGCTCTCCAGGAAAGCTCAAGCT 669
QY 121 GlyGly-----ValPhePheIleLeuGlyIleLeuGlyIleLeuGlyIleProVal 137
DB 670 GCGCGCCACCGCAGGCGCTTCCACATCTGCGCGGTATCTGCGGATGATGCGCATCTCC 729
QY 138 TrpAsnLeuHisGlyIleLeuArgAspPheTySerProLeuValProAspSerMet 157
DB 730 TGGTACCGCTTCAACATACCCGGGACTTCTTCAACCCCTTGTATCCCGGAAAC--AAG 786
QY 158 PheGluIleGlyGlnAlaLeuTyLeuGlyIleIleSerSerLeuPheSerLeuIleAla 177
DB 787 TAGGAGTGGGCCCCCGCTTACTGCGGTGAGAGCCCTCACATCTCATCTCGGT 846
QY 178 GlyIleIleLeuCysPheSerCys-----SerSerGlnArgAsnArgSerAsnTy 194
DB 847 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
QY 195 TyrAspAlaTyrglnAla-----GlnProLeuAlaThrArgSerProArg 210
DB 907 CGCGCGCCCTTACAGGCTCCAGTCCGATGATGCCCGCTGCGCACC-----TCGAGCA 960
QY 211 ProGlyGlnProProlyValIleSerGlnPheAsnSerTySerLeuThrGlyTyVal 230
DB 961 GAAGGCGAC-----AGCAGCTTGGCAATACGCGCAAGAAAGCCTAGGTG 1005

RESULT 14
US-09-724-864-32
; Sequence 32, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.105001
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Mouse
US-09-724-864-32

Alignment Scores:
Pred. No.: 1,74e-25 Length: 1353
Score: 275.00 Matches: 62
Percent Similarity: 48.46% Conservative: 48
Best Local Similarity: 27.31% Mismatches: 101
Query Match: 23.42% Indels: 16

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DB: 3 Gaps: 4
US-09-787-677a-3 (1-230) x US-09-724-864-32 (1-1353)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyTrpIleLeuGlyLeuLeuGlyLeu 20
DB 136 ATGCGCCACCAACGATGCGAGGTGTGAGGCTTCTCTGCTCCCTCGGCTGCGCGGC 195
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpIleThrSerSerTyValAlaSerIle 40
DB 196 TGCATACCCCTGAGTGGAGTGAACATGTGAGAGCACTCAAGACCTGTATGAC--ACC 252
QY 41 ValThrAlaValGlyPheSerTyGlyLeuTrpMetGluCysAlaThrHisSerThyl 60
DB 253 GTCAACCCCTGTTTCCAGCATGAGAGGCTTGTGAGAGAGTTCCTGCAACAGAGCTGGG 312
QY 61 IleThrGlnCysAspIleTySerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
DB 313 TTCACCGAGTGGCGGCATCTTCAACATCTGCGCTTCCAGCATGCTGCAAGCTGTA 372
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 373 CGAGCCCTGATGATCGTGGGCACTTCTGCGGAGTCACTCGGTATCTCTGCTCATCTTC 432
QY 101 GlyMetArgCys--ThrValPheCysGlnGluSerArgAlaIleAspArgValAlaVal 119
DB 433 GCGCTGAGTGCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATG 492
QY 120 AlaGlyIleValPhePheIleLeuGlyIleLeuGlyIlePheIleProValAla----- 137
DB 493 ACTTGTGGATCTTGTTCATCATCTCCGCGCATCTGTCATCATCTGCTGTGTTT 552
QY 138 -----Trp-----AsnLeuHisGlyIleLeuArg 145
DB 553 GCCAATGCTGTGTGACCACTTCTGATGTCCACAGTAACTGATGACAGCGGAGTGC 612
QY 146 AspPheTySerProLeuValProAspSerMetLeuPheGluIleGlyGlnAlaLeuTy 165
DB 613 GGCATGCTGCGCATGCGTGCAGACCTTCAACAGATGACACTTGGTGCAGCTCTTTC 672
QY 166 LeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIleLeuCysPheSerCys 185
DB 673 GTGGGCTGGTGTCTGAGAGCTTCAACCTGATGAGGAGTGTGATGATGATGATGATG 732
QY 186 SerSerGlnArgAsnArgSerAsnTyTrpAspAlaTyrglnAlaGlnProLeuAlaThr 205
DB 733 CTGGGCTGACACCAATGACAGCACTTCAAGCTGTGCTTACCATGCGCTGCGCAA 792
QY 206 ArgSerSerProArgProGly 212
DB 793 AATGTCCTTACAGGCTTGA 813

RESULT 15
US-08-966-316-8
; Sequence 8, Application US/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murty, Lynn E.
; APPLICANT: Mathur, Preeti
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```



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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS Windows Version 2.0
SOFTWARE: FASTSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HMTJAZT01
CLONE: 2417676
US-08-966-316-8

Alignment Scores:
Pred. No.: 7.75e-21 Length: 363
Score: 232.00 Matches: 44
Percent Similarity: 63.81% Conservative: 23
Best Local Similarity: 41.90% Mismatches: 38
Query Match: 19.76% Indels: 0
DB: 2 Gaps: 0

US-09-787-677A-3 (1-230) x US-08-966-316-8 (1-363)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly 20
Db 48 ATGGCCCTCTGCCGAAATGCAATCTCTGGAGTCTCTGACACTGCTGGGCTGGTAAT 107
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrIleThrSerSerTyrValGlyAlaSerIle 40
Db 108 GGCCTGGTCTCTGTCGCCCTGCGCATGTGAGAGGTGACCGCTTCATCGGCAACAGCATC 167
QY 41 ValThrAlaValAlaGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
Db 168 GTGGTGCCCGAGGTGGTGGAGGGCTGTGATGTCCTGCTGTGCAGAGCACCGGC 227
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db 228 CAGATGCAAGTGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 287
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 288 CGTGCCCTCTGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 347
QY 101 GlyMetArgCysThr 105
Db 348 GGGGCCAAGTTTACC 362
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Search completed: December 20, 2004, 16:51:58
Job time : 98 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 15:38:36 ; Search time 546 Seconds
(without alignments)
2325.628 Million cell updates/sec

Title: US-09-787-677A-3
Perfect score: 1174
Sequence: 1 MASLGLVYVIGLILGLLG.....PCGPVKSEFNSYSILTVY 230

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 6186004

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-CGN2_1/USPTO.spool/US09787677.rnuc 20122004.132742.19497/app.query.fasta_1.391
-DB=Published Applications NA -QFMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09787677 @CGN 1 1 480 @rnuc 20122004.132742.19497
-NCPU=6 -ICPU=3 -NO_MMAP -LARGESQUERY -NEG_SCORES=0 -MAIT -DSBLOC=100
-LONGLOG -DEV TIMEOUT=120 -MARS TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	1400	11 US-09-978-360A-56	Sequence 56, App1
2	1174	100.0	1400	10 US-10-319-763-139	Sequence 139, App
3	1174	100.0	1475	10 US-09-888-257A-1	Sequence 1, App1
4	1174	100.0	1475	10 US-09-946-374-133	Sequence 133, App
5	1174	100.0	1475	13 US-10-006-867-79	Sequence 79, App1
6	1174	100.0	1475	13 US-10-063-547-79	Sequence 79, App1
7	1174	100.0	1475	13 US-10-063-551-79	Sequence 79, App1
8	1174	100.0	1475	13 US-10-028-072-491	Sequence 491, App
9	1174	100.0	1475	14 US-10-063-616-79	Sequence 79, App1
10	1174	100.0	1475	14 US-10-140-808-491	Sequence 491, App
11	1174	100.0	1475	14 US-10-063-589-79	Sequence 79, App1
12	1174	100.0	1475	14 US-10-063-513-79	Sequence 79, App1
13	1174	100.0	1475	14 US-10-063-515-79	Sequence 79, App1
14	1174	100.0	1475	14 US-10-063-512-79	Sequence 79, App1
15	1174	100.0	1475	14 US-10-121-049-491	Sequence 491, App
16	1174	100.0	1475	14 US-10-123-904-491	Sequence 491, App
17	1174	100.0	1475	14 US-10-140-470-491	Sequence 491, App
18	1174	100.0	1475	14 US-10-063-502-79	Sequence 79, App1
19	1174	100.0	1475	14 US-10-175-746-491	Sequence 491, App
20	1174	100.0	1475	14 US-10-176-918-491	Sequence 491, App
21	1174	100.0	1475	14 US-10-176-921-491	Sequence 491, App
22	1174	100.0	1475	14 US-10-063-548-79	Sequence 79, App1
23	1174	100.0	1475	14 US-10-137-865-491	Sequence 491, App
24	1174	100.0	1475	14 US-10-140-474-491	Sequence 491, App
25	1174	100.0	1475	14 US-10-142-431-491	Sequence 491, App
26	1174	100.0	1475	14 US-10-143-114-491	Sequence 491, App
27	1174	100.0	1475	14 US-10-140-002-491	Sequence 491, App
28	1174	100.0	1475	14 US-10-063-554-79	Sequence 79, App1
29	1174	100.0	1475	14 US-10-006-856A-133	Sequence 133, App
30	1174	100.0	1475	14 US-10-142-419-491	Sequence 491, App
31	1174	100.0	1475	14 US-10-063-553-79	Sequence 79, App1
32	1174	100.0	1475	14 US-10-063-518-79	Sequence 79, App1
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42	1174	100.0	1475	14 US-10-006-485A-133	Sequence 133, App
43	1174	100.0	1475	14 US-10-013-907A-133	Sequence 133, App
44	1174	100.0	1475	14 US-10-015-499A-133	Sequence 133, App
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ALIGNMENTS

RESULT 1
US-09-978-360A-56
Sequence 56, Application US/0978360A
Publication No. US20040110939A1
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste Dumas Mline
APPLICANT: Bougueleret, Lydie
APPLICANT: Joubert, Severin
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56. US4.CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/081,563

PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR FILING DATE: -09-04
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1999-02-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent.pm
SEQ ID NO 56
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 36..107
OTHER INFORMATION: Von Heljne matrix
OTHER INFORMATION: score 5.6999980926514
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1302..1307
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1389..1400
US-09-978-360A-56

Alignment Scores:
Pred. No.: 2,26e-131 Length: 1400
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-978-360A-56 (1-1400)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB 36 ATGGCTCTCTGGCTCCCACTTGTGGCTACATCCAGGCTTTCTGGGCTTTTGGGC 95
QY 21 ThrLeuValAlaMetLeuLeuProSerTrrPheSerTrrValGlyAlaSerIle 40
DB 96 ACACGTGTTGCATGCTGCTCCAGCTGGAAACAAAGTTTATGTGCGGCAAGCAT 155
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrrMetGlyCysAlaThrHisSerThrGly 60
DB 156 GTGACAGCAGTGTGCTTCTCCAGGCTCTGATGATGATGTCACACACAGCAGGC 215
QY 61 IleThrGlnCysAspIleTrrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
DB 216 ATCCACCAAGTGTGATCTATAGCACCTTGTGGCTGCGCGGTGACATCCAGGCTGCC 275
QY 81 GlnAlaMetLeuValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 276 CAGGCTCATGATGGAGCATCCAGTCAATCTCCCTGGCTGCTCATTTATCTGTGGTG 335
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerAlaValAspAlaValAla 120
DB 336 GGGCTGTGAGTGCACAGCTTCTGTCAGGAATCCGAGCCAAAGACAGGTGGCGTAC 395
QY 121 GlyGlyValPhePheIleLeuGlyLeuLeuGlyPheIleProValAlaTrrAsnLeu 140
DB 396 GGTGGAGTCTTTTCTTCTGAGGCTCTGAGGATTCCTGTTGCTGGAATCTT 455
QY 141 HisGlyIleLeuArgAspPheTrrSerProLeuValProAspSerMetLysPheGluIle 160

DB 456 CATGGATCTTACGGGCTTCTACTCACCACTGTGCTTACAGCATGAATTTGAGATT 515
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DB 516 GGAAGAGCTTTTACTTGGGCTATTTCTTCCCTGTTCCCTGATGCTGGATCATC 575
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DB 576 CTCTGCTTTTCCCTGCTATATCCAGAGAAATCGCTCCAACTACATGCTTACCAAGCC 635
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 636 CAACCTTGTCCCAAGAGACCTCTCCAAAGGCTGTGTCACCTCCAAAGTCAAGAGTAC 695
QY 221 PheAsnSerTrrSerLeuThrGlyTrrVal 230
DB 696 TTCAATTCCTTACAGCTGACAGGATATGTG 725

RESULT 2

US-10-319-763-139
Sequence 139, Application US/10319763
Publication No. US20030144490A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducleret, Aymeric
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: G-031.US04.DIV
CURRENT APPLICATION NUMBER: US/10/319,763
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 139
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 36..107
OTHER INFORMATION: Von Heljne matrix
OTHER INFORMATION: score 5.6999980926514
OTHER INFORMATION: seq ILGLLGLTLVA/ML
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1302..1307
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1389..1400
US-10-319-763-139

Alignment Scores:
Pred. No.: 2,26e-131 Length: 1400
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-787-677A-3 (1-230) x US-10-319-763-139 (1-1400)

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QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB 36 ATGGCTCTCTTGGCTTCCAACTTGTGGCTACATCTTAGCCCTTGGGGCTTTGGGC 95
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle 40
DB 96 ACCTGGTTGCCATGCTGCTCCCAAGTGAAGAAACAAAGTTCTTATGTCGGTGCAGATT 155
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThgLy 60
DB 156 GTGACGACAGTTCCTTCCAAAGGCTCTGGATGGAATGTCCACACAGACAGCAGGC 215
QY 61 IleThrGlnCysAspIleTySerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
DB 216 ATACACCAAGTGTACATCTATAGCACCTTCTGGGCTGCCCCCTGACATCCAGGCTGCC 275
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 276 CAGGCATGATGTGTGACATCCAGTGCATCTCTCCCTGCGCTGCATATCTCTGTGCTG 335
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
DB 336 GGCATGAGATGCACAGCTCTTCCCAAGAAATCCCAAGCAAGACAGAGTGGCGTAGCA 395
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTrpAsnLeu 140
DB 396 GGTGGAGTCTTTTTCATCTTGAAGGCTCTTGGGATTCATTCCTGTGCTGGAATCTT 455
QY 141 HisGlyIleLeuArgAspPheTySerProLeuValProAspSerMetLysPheGluIle 160
DB 456 CATTGGATCTTACGGGACTTCTACTACCACTGCTGCTACAGCATGAATTTGAGATT 515
QY 161 GlyGlyAlaLeuTyLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 516 GGAGAGCTCTTACTTGGGCTTATTTCTCCCTGTTCTCCCTGATGAGTGAATCATC 575
QY 181 LeuCysPheSerCysSerSerGlnArgAspArgSerAsnTyTrpAspAlaTyArgAla 200
DB 576 CTCTGCTTTTCCGCTCATCTCCAGAGAAATGCTCCCAACTACATACGATGCTTCCAA 635
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 636 CAACCTCTTGCCCAAGAGAGCTCTCCAGGCTGTGTAACCTCCCAAGTCAAGAGTGA 695
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RESULT 3

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US-09-888-257A-1
/ Sequence 1, Application US/09888257A
/ Publication No. US20030060612A1
/ GENERAL INFORMATION:
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Polakis, Paul
/ APPLICANT: Smith, Victoria
/ APPLICANT: Wood, William I.
/ APPLICANT: Wu, Thomas D.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
/ FILE REFERENCE: P5002R1
/ CURRENT APPLICATION NUMBER: US/09/888,257A
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/063,540
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: US 60/089,653
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: US 60/099,792
/ PRIOR FILING DATE: 1998-09-10

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/ PRIOR APPLICATION NUMBER: US 60/103,678
/ PRIOR FILING DATE: 1998-10-08
/ PRIOR APPLICATION NUMBER: US 60/235,451
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: PCT/US99/12252
/ PRIOR FILING DATE: 1999-06-02
/ PRIOR APPLICATION NUMBER: PCT/US99/20111
/ PRIOR FILING DATE: 1999-09-01
/ PRIOR APPLICATION NUMBER: PCT/US00/04342
/ PRIOR FILING DATE: 2000-02-18
/ PRIOR APPLICATION NUMBER: PCT/US00/05841
/ PRIOR FILING DATE: 2000-03-02
/ PRIOR APPLICATION NUMBER: PCT/US00/08439
/ PRIOR FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: PCT/US00/23328
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: PCT/US00/32678
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US01/06520
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: PCT/US01/06666
/ PRIOR FILING DATE: 2001-03-01
/ NUMBER OF SEQ ID NOS: 10
/ SEQ ID NO 1
/ LENGTH: 1475
/ TYPE: DNA
/ ORGANISM: Homo Sapien
/ US-09-888-257A-1

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Alignment Scores:

Pred. No.:	2,43e-131	Length:	1475
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

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US-09-787-677A-3 (1-230) x US-09-888-257A-1 (1-1475)
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DB 122 ATGGCTCTCTTGGCTTCCAACTTGTGGCTACATCTTAGCCCTTGGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle 40
DB 182 ACCTGGTTGCCATGCTGCTCCCAAGTGAAGAAACAAAGTTCTTATGTCGGTGCAGATT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThgLy 60
DB 242 GTGACGACAGTTCCTTCCAAAGGCTCTGGATGGAATGTCCACACAGACAGCAGGC 301
QY 61 IleThrGlnCysAspIleTySerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
DB 302 ATACACCAAGTGTACATCTATAGCACCTTCTGGGCTGCCCCCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCATGATGTGTGACATCCAGTGCATCTCTCCCTGCGCTGCATATCTCTGTGCTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
DB 422 GGCATGAGATGCACAGTCTTCTGCAAGAAATCCCAAGCAAGACAGAGTGGCGTAGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTrpAsnLeu 140
DB 482 GGTGGAGTCTTTTTCATCTTGAAGGCTCTGGAATTCATTCCTGTGCTGGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTySerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CATTGGATCTTACGGGACTTCTACTACCACTGCTGCTGCAAGCATGAATTTGAGATT 601
QY 161 GlyGlyAlaLeuTyLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180

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Db 602 GGAGAGCTCTTACTTGCGCATTTATTTCTCCCTGTTCCCTGATAGTCGATCATC 661
Qy 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAntYrTyraAlaIYrGlnAla 200
Db 662 CTCTGCTTTTCCGCTCATCTCCAGAAATCGCTCCCACTACTACATGCTTCCAGGCC 721
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
Db 722 CAACCTCTTGCCACAGAGACTCTCCAGGCTTGCTCAACCTCCCAAGTCAGAGTGTAG 781
Qy 221 PheAsnSerTySerLeuThrGlyTyVal 230
Db 782 TTCAATTCCTACAGCTCGACAGGCTATGTG 811
RESULT 4
US-09-946-374-133
Sequence 133, Application US/09946374
Publication No. US2003073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
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PRIOR APPLICATION NUMBER: 60/098750
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PRIOR FILING DATE: 1998-09-10
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PRIOR FILING DATE: 1998-09-10

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PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103328
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PRIOR APPLICATION NUMBER: 60/103395
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PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
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PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores: 2.43e-131 Length: 1475
Pred. No.:

Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-787-677a-3 (1-230) x US-09-946-374-133 (1-1475)

QY 1 MetAlaSerLeuGlnLeuValGlyTyrIleLeuGlnLeuGlyLeuGly 20
122 ATGGCCCTCTTGGCCCTCACTTGGCTTACATCCCTTGGGGCTTTGGG 181
QY 21 ThrLeuValAlaMetLeuProSerTyrLeuSerTyrValGlyAlaSerIle 40
182 ACACGTGTGCGACGTGCTCCAGCTGGAACAAAGTCTTAATGCGGAGCAT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThy 60
242 GTGACAGCACTTGGCTTCTCCAGGGCTCTGATGGAATGTCACACAGACAGC 301
QY 61 IleThrGlnCysApIleTyrSerThrLeuGlnGlyLeuProAlaApIleGlnAla 80
302 ATCACCAGTGTACATCTATACACCTTCTGGGCTGCGCTGACATCCAGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
362 CAGGCCATGATGATGATCATCATCATCTCTCCCTGCGCATATCTCTGTGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaValAla 120
422 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
QY 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTyrAsnLeu 140
482 GGTGAGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 541
QY 141 HisGlyIleLeuArgPheTyrSerProLeuValProAspSerMetLeuPheGluIle 160
542 CATGGATCTTCAAGGATCTTCAAGGATCTTCAAGGATCTTCAAGGATCTTCAAGG 601
QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaIleIle 180
602 GAGAGGCTCTTACTTGGGCTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 661
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
662 CTCGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlyValIleSerGlu 220
722 CAACCTCTTGGCCCAAGAGCTTCCAAAGGCTGTCAACCTTCCAAAGTCAAGAGT 781
QY 221 PheAsnSerTyrSerLeuThyVal 230
782 TTCAATTCCTACAGCTGACAGGGTATGTG 811

RESULT 5
US-10-006-867-79
; Sequence 79, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: WOOD, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1

CURRENT APPLICATION NUMBER: US/10/006,867
PRIOR FILING DATE: 2001-12-06
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PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/064215
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PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089514
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PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114223
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 60/115614
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116527
PRIOR FILING DATE: 1999-01-20

QY 61 IIEThGInCYsaAppliETyRSerThrLeuEngLYleuProAlaAppliEGInAlaAla 80
DB 302 ATACCCAGGTGATGACATCTAATAGACACCTTCTGGGCGCTGCGGTGACATCCAGCGTGGC 361
QY 81 G1AlaMetMetVal1ThrSerSerAla1IleSerSerLeuAlaCYsIleIleSerVal1 100
DB 362 CAGGCCATGATGGATGACATCCAGTGCATCTCTCCCTGGCGCTGATTAATCTCTGTGTG 421
QY 101 GlyMetArgCYThrVal1PheCYeGInGluSerArgAlaIuYsApPaTgVal1AlaVal1Ala 120
DB 422 GGCATGATGATGACATGCTTCTGCGCAGGAATCCGAGCCAAAGACAGATGGCGGTAGCA 481
QY 121 G1G1YVal1PhePheIleLeuG1YgLYleuEngLYPheIleProVal1AlaTPAsnLeu 140
DB 482 GGTGAGATCTTTTTCATCTTGGAGGCTCTGAGGATTCATCTGTTGCTGGAATCTT 541
QY 141 H1eG1YIleLeuArgApPheTyRSerProLeuVal1ProAspSerMetLYsPheGluIle 160
DB 542 CATGGATCTTACGGGACTTCTACTCACACTGCTGCTGACATGAAATTTGAGATT 601
QY 161 G1YGLuAlaLeuTyRleuG1YIleIleSerSerLeuPheSerLeuIleAlaG1YIleIle 180
DB 602 GGAAGAGCTCTTACTTGGGATTAATTTCTTCTGTTCTGCTGATAGCTGAATCATC 661
QY 181 LeuCYsPheSerCYsSerSerGlnArgAsnArgSerAntyTyRAspAlaTyRGLuAla 200
DB 662 CTCTGCTTTTCCGCTCATCCAGAGAAATGCTCCAACTACATGATGCTTACCAAGCC 721
QY 201 G1nProLeuAlaThrArgSerSerProArgProG1YgInProPolysVal1YsSerGlu 220
DB 722 CAACCTTTGCCCAAGAGCTCTCCAAAGCGCTGTCACTCCCAAGTCAAGAGTGG 781
QY 221 PheAsnSerTyRSerLeuThrG1YTyRVal 230
DB 782 TTCATTTCTTACAGCTGACAGCGGTATGTG 811

RESULT 7

US-10-063-551-79

; Sequence 79, Application US/10063551

; Publication No. US20020183494A1

; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.

; APPLICANT: Gerriksen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Matanabe, Colin K.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3230R1C1

; CURRENT APPLICATION NUMBER: US/10/063, 551

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 170

; SEQ ID NO 79

; LENGTH: 1475

; TYPE: DNA

; ORGANISM: Homo Sapien

; US-10-063-551-79

Alignment Scores:

Pred. No.: 2,43e-131

Score: 1174.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 13

Length: 1475

Matches: 230

Conservative: 0

Mismatch: 0

Indels: 0

Gaps: 0

US-09-787-677A-3 (1-230) X US-10-063-551-79 (1-1475)

QY 1 MetAlaSerLeuG1YleuG1nLeuVal1G1YTyR1IleuEngLYleuEngLYleuEngLY 20
DB 122 ATGGCTCTTCTTGGCTTCACTTATGAGGCTTACATCTTACAGCTTCTTGGGCTTTTGGG 181
QY 21 ThrLeuVal1AlaMetLeuLeuProSerTrpLYsThrSerSerTyRVal1G1YAlaSerIle 40
DB 182 ACATGCTTCCATGCTGCTTCCAGCTGAGAAAACAAGTTCTTATGCGGTGCAGCAT 241
QY 41 Val1ThrAlaVal1G1YPheSerLYeG1YleuTyRMetG1uCYsAlaThrHisSerThyGly 60
DB 242 GTGACAGCATTTGCTTCTTCCAGGCGCTTGTGATGGAATGTCACACACAGCAGCGG 301
QY 61 IIEThGInCYsaAppliETyRSerThrLeuEngLYleuProAlaAppliEGInAlaAla 80
DB 302 ATACCCAGGTGATGACATCTAATAGACACCTTCTGGGCGCTGCGGTGACATCCAGCGTGGC 361
QY 81 G1AlaMetMetVal1ThrSerSerAla1IleSerSerLeuAlaCYsIleIleSerVal1 100
DB 362 CAGGCCATGATGGATGACATCCAGTGCATCTCTCCCTGGCGCTGATTAATCTCTGTGTG 421
QY 101 GlyMetArgCYThrVal1PheCYeGInGluSerArgAlaIuYsApPaTgVal1AlaVal1Ala 120
DB 422 GGCATGATGATGACATGCTTCTGCGCAGGAATCCGAGCCAAAGACAGATGGCGGTAGCA 481
QY 121 G1YGLuAlaLeuTyRleuG1YIleIleSerSerLeuPheSerLeuIleAlaG1YIleIle 140
DB 482 GGTGAGATCTTTTTCATCTTGGAGGCTCTGAGGATTCATCTGTTGCTGGAATCTT 541
QY 141 H1eG1YIleLeuArgApPheTyRSerProLeuVal1ProAspSerMetLYsPheGluIle 160
DB 542 CATGGATCTTACGGGACTTCTACTCACACTGCTGCTGACATGAAATTTGAGATT 601
QY 161 G1YGLuAlaLeuTyRleuG1YIleIleSerSerLeuPheSerLeuIleAlaG1YIleIle 180
DB 602 GGAAGAGCTCTTACTTGGGATTAATTTCTTCTGTTCTGCTGATAGCTGAATCATC 661
QY 181 LeuCYsPheSerCYsSerSerGlnArgAsnArgSerAntyTyRAspAlaTyRGLuAla 200
DB 662 CTCTGCTTTTCCGCTCATCCAGAGAAATGCTCCAACTACATGATGCTTACCAAGCC 721
QY 201 G1nProLeuAlaThrArgSerSerProArgProG1YgInProPolysVal1YsSerGlu 220
DB 722 CAACCTTTGCCCAAGAGCTCTCCAAAGCGCTGTCACTCCCAAGTCAAGAGTGG 781
QY 221 PheAsnSerTyRSerLeuThrG1YTyRVal 230
DB 782 TTCATTTCTTACAGCTGACAGCGGTATGTG 811

RESULT 8

US-10-028-072-491

; Sequence 491, Application US/10028072

; Publication No. US20030004311A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerriksen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin L.

; APPLICANT: Matanabe, Colin K.

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; APPLICANT: Zhang

; TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

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Alignment Scores:
Pred. No.:      2,43e-131      Length:      1475
Score:          1174.00        Matches:      230
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%       Indels: 0
DB:             14            Gaps: 0

```

US-09-787-677a-3 (1-230) x US-10-028-072-491 (1-1475)

```

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB 122 ATGGCCCTCTTGCCCTCCACCTTGCGCTACATCTTAGGCTTTGGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle 40
DB 182 ACACTGGTTGCCAGTGCCTCCAGCGGAAACAAAGTTCTTATGTCGGTCCAGCATTT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGlyCysValAlaThrHisSerThrGly 60
DB 242 GTGACACAGATGGCTTCTCCAAAGGCTCTGATGGATGTGCACACACAGACAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
DB 302 ATCACCCAGTGTACATCTATAGCACCCCTTGAGGCTGCCCGCTGACATCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCCATGATGAGATCATCCAGTCAATCTCCCTCGGCTGCATTATCTGTGGTG 421
QY 101 GlyMetArgCysTrpValPheCysGlnGlySerTrpAlaValAspAlaValAlaAla 120
DB 422 GGCACTGAGATGCACAGCTCTCTCCAGGAATCCGAGCAAAAGACAGATGGCGGTAGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaAlaTrpAsnLeu 140
DB 482 GGTGAGATCTTTTCACTTCCTTGAGGCTCTCGGGAATTCATCTCGTGGCTGGAAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160

```

```

DB 542 CATGGATCTTACGGGCTTCTACTACACACATGTCCTGACAGCATGAATTTGAGATT 601
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 602 GGAAGGCTCTTACTTGGGCAATTATTTCTCCCTGTTCTCCCTGATAGCTGGAAATCATC 661
QY 181 LeuCysePheSerCysSerSerGlnArgAsnArgSerAsnTyrTyraAspAlaTyrglnAla 200
DB 662 CTCTGCTTTTCCCTGCTATATCCAGAGAAATCGCTCCAACTACATACATGCTCCAAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
DB 722 CAACCTCTTCCCAAGAGACTCTCCAAAGGCTGTGTCAACCTCCCAAGTCAAGAGTGAAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCAAATTCCTAACGCTTGACAGGGGTATGTG 811

```

RESULT 9

```

; US-10-063-616-79
; Sequence 79, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Paim
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-063-616-79

```

```

Alignment Scores:
Pred. No.:      2,43e-131      Length:      1475
Score:          1174.00        Matches:      230
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%       Indels: 0
DB:             14            Gaps: 0

```

US-09-787-677a-3 (1-230) x US-10-063-616-79 (1-1475)

```

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB 122 ATGGCCCTCTTGCCCTCCACCTTGCGCTACATCTTAGGCTTTGGGGCTTTTGCGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle 40
DB 182 ACACTGGTTGCCAGTGCCTCCAGCGTGAACAAAGTTCTTATGTCGGTCCAGCATTT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGlyCysValAlaThrHisSerThrGly 60
DB 242 GTGACACAGATGGCTTCTCCAAAGGCTCTGATGGAAATGTGCACACACAGACAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
DB 302 ATCACCCAGTGTACATCTATAGCACCCCTTGAGGCTGCCCGCTGACATCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100

```

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Db      362 CAGGCCATGATGGTGAATCAGTGCATCTCCTCGGCGTGCATATATCTGTGTG 421
Qy      101 GYMeArGcYsThrValPheCySGInGluSerArgAlaIysAspArgValAlaValAla 120
Db      422 GGCATGAGATGCACAGCTCTTCTCCAGGAATCCCGAGCCAAAGACAGAGTGGCGTAGCA 481
Qy      121 GYGLVAlPhePheIleuGlyGlyLeuGlyGlyPheIleProValAlaTPanLeu 140
Db      482 GGTGGAGCTTTTTCATCTTGAGAGGCTCTGGATTCCTCTGTGGCTTGGAACTT 541
Qy      141 HIsGLYIleuArgAspPheTySerProLeuValProAspSerMetLysPheGluIle 160
Db      542 CATGGATCCTTAGGGAGCTTCTACTCAACACTGGTGTCAAGCATGAATTTAGATT 601
Qy      161 GYGLVAlaLeuTyrluGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db      602 GGAGAGGCTTTTACTGGGCAATTAATTTCTCCCTGTTCTCCCTGATGAGTCGAATCATC 661
Qy      181 LeuCySPheSerCySerSerGlnArgAspArgSerAsnTyrlTyrlAspAlaTyrlGlnAla 200
Db      662 CTCTGCTTTTCCGCTCATCCAGAGAAATCGCTCCAACTACACTACGATGCTTCAAGCC 721
Qy      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db      722 CAACCTCTTGCCCAAGAGAGCTCTCCAGGCGCTGTCAACCTCCCAAGTCAGAGTGAAG 781
Qy      221 PheAsnSerTySerLeuThrGlyTyrlVal 230
Db      782 TTCATATTCTACAGCTGACAGGGTATGTG 811

```

RESULT 10

```

US-10-140-808-491
; Sequence 491, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; PRIOR APPLICATION DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 491
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-808-491

```

Alignment Scores:

```

Pred. No.: 2,43e-131 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

```

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US-09-787-677a-3 (1-230) x US-10-140-808-491 (1-1475)

```

```

Qy      1 MeAlSerLeuGlyLeuGlnLeuValGlyTyrlIleuGlyLeuLeuGlyLeuLeuGly 20
Db      122 ATGGCTCTCTTGGCTCCCAACTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGC 181
Qy      21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrlValGlyAlaSerIle 40
Db      182 ACACGTGGTGCAGTGGCTGCTCCACAGTGAAGAAACAAAGTTCTTATGTGGTGCAGCAT 241
Qy      41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db      242 GTACACAGAGTTGGCTTCTTCCAAAGGCGCTCTGGATGGAATGTCCACACACACACAGGC 301
Qy      61 IleThrGlnCySPheAspIleTySerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db      302 ATCACCAGATGTACATCTATACACACTTCTGGGCGTGGCCGCTGACATCCAGGCTGCC 361
Qy      81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db      362 CAGGCCATGATGGTGAATCCAGTGCATCTCCTCGGCGTGCATATCTGTGTG 421
Qy      101 GYMeArGcYsThrValPheCySGInGluSerArgAlaIysAspArgValAlaValAla 120
Db      422 GGCATGAGATGCACAGCTCTTCTCCAGGAATCCCGAGCCAAAGACAGAGTGGCGTAGCA 481
Qy      121 GYGLVAlPhePheIleuGlyGlyLeuGlyGlyPheIleProValAlaTPanLeu 140
Db      482 GGTGGAGCTTTTTCATCTTGAGAGGCTCTCGGATTCATTCCTGTGCTGGAACTT 541
Qy      141 HIsGLYIleuArgAspPheTySerProLeuValProAspSerMetLysPheGluIle 160
Db      542 CATGGATCCTTAGGGAGCTTCTACTCAACACTGGTGTCAAGCATGAATTTAGATT 601
Qy      161 GYGLVAlaLeuTyrluGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db      602 GGAGAGGCTTTTACTTGGGCAATTAATTTCTCCCTGTTCTCCCTGATGAGTCGAATCATC 661
Qy      181 LeuCySPheSerCySerSerGlnArgAspArgSerAsnTyrlTyrlAspAlaTyrlGlnAla 200
Db      662 CTCTGCTTTTCCGCTCATCCAGAGAAATCGCTCCAACTACACTACGATGCTTCAAGCC 721
Qy      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db      722 CAACCTCTTGCCCAAGAGAGCTCTCCAGGCGCTGTCAACCTCCCAAGTCAGAGTGAAG 781
Qy      221 PheAsnSerTySerLeuThrGlyTyrlVal 230
Db      782 TTCATATTCTACAGCTGACAGGGTATGTG 811

```

RESULT 11

```

US-10-063-569-79
; Sequence 79, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3320R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; PRIOR APPLICATION DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475

```

```

; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-569-79

Alignment Scores:
Pred. No.: 2,43e-131      Length: 1475
Score: 1174.00           Matches: 230
Percent Similarity: 100.00%  Conservaive: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 14                   Gaps: 0

US-09-787-677a-3 (1-230) x US-10-063-569-79 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 122 ATGGCCCTCTTGGCTCCCACTGTGGCTACATCTCAGGCTTCTGGGGCTTTTGGGC 181

QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysSerSerTrpValGlyAlaSerIle 40
Db 182 ACACGTGTTGCCATGCTGCTCCCACTGGAAACAAAGTTCTTATGTCGGTCCAGCATT 241

QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
Db 242 GTGACACAGATGGCTTCTCCAAAGGCTCTGATGGAATGGCACACACAGCAGCAGGC 301

QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlnGlyLeuProAlaAspIleGlnAlaAla 80
Db 302 ATACCCAGATGATGATCATCTATAGCACCCCTTCTGGGCTGACATCCAGGCTGCC 361

QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGATGATCATCTATAGCACCCCTTCTGGGCTGACATCCAGGCTGCC 421

QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
Db 422 GGCATGAGATGACAGCTCTTCTCCAGGAATCCGAGCNAAGACAGATGGCGGTAGCA 481

QY 121 GlyGlyValAlaPhePheIleLeuGlyGlyLeuGlnGlyPheIleProValAlaTrpAsnLeu 140
Db 482 GGTGAGATCTTTTTCATCTTGGAGGCTCTGGAATTCATCTCTGTTGCTGGAACTTT 541

QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
Db 542 CATGGATCTCTACGGGACTTCTACTACCACTGGTGCCTGACACAGAAATTTGAGATT 601

QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAGAGGCTCTTACTTGGGCAATATTCTTCCCTGTTCTCCGATAGCTGGAATCATC 661

QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCTGCTCATCTCCAGAAATGCTCCAACTACAGATGCTTACCAAGCC 721

QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGln 220
Db 722 CAACCTTTTGGCACAAGAGCTCTCCAAAGCTGTGCTCACTCCCAAGTCAAGAGTGA 781

QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCAATTCTTACAGCTGACAGGCTATGTG 811

RESULT 12
US-10-063-513-79
; Sequence 79, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Elivaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

```

```

; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; PRIORITY FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-79

Alignment Scores:
Pred. No.: 2,43e-131      Length: 1475
Score: 1174.00           Matches: 230
Percent Similarity: 100.00%  Conservaive: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 14                   Gaps: 0

US-09-787-677a-3 (1-230) x US-10-063-513-79 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 122 ATGGCCCTCTTGGCTCCCACTGTGGCTACATCTCAGGCTTCTGGGGCTTTTGGGC 181

QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysSerSerTrpValGlyAlaSerIle 40
Db 182 ACACGTGTTGCCATGCTGCTCCCACTGGAAACAAAGTTCTTATGTCGGTCCAGCATT 241

QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
Db 242 GTGACACAGATGGCTTCTCCAAAGGCTCTGATGGAATGGCACACACAGCAGCAGGC 301

QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlnGlyLeuProAlaAspIleGlnAlaAla 80
Db 302 ATACCCAGATGATGATCATCTATAGCACCCCTTCTGGGCTGACATCCAGGCTGCC 361

QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGATGATCATCTATAGCACCCCTTCTGGGCTGACATCCAGGCTGCC 421

QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
Db 422 GGCATGAGATGACAGCTCTTCTCCAGGAATCCGAGCNAAGACAGATGGCGGTAGCA 481

QY 121 GlyGlyValAlaPhePheIleLeuGlyGlyLeuGlnGlyPheIleProValAlaTrpAsnLeu 140
Db 482 GGTGAGATCTTTTTCATCTTGGAGGCTCTGGAATTCATCTCTGTTGCTGGAACTTT 541

QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
Db 542 CATGGATCTCTACGGGACTTCTACTACCACTGGTGCCTGACACAGAAATTTGAGATT 601

QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAGAGGCTCTTACTTGGGCAATATTCTTCCCTGTTCTCCGATAGCTGGAATCATC 661

QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCTGCTCATCTCCAGAAATGCTCCAACTACAGATGCTTACCAAGCC 721

QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGln 220
Db 722 CAACCTTTTGGCACAAGAGCTCTCCAAAGCTGTGCTCACTCCCAAGTCAAGAGTGA 781

QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCAATTCTTACAGCTGACAGGCTATGTG 811

```

```
RESULT 13
US-10-063-515-79
; Sequence 79, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION: 2002-05-01
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-515-79

Alignment Scores:
Pred. No.: 2,43e-131 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-787-677a-3 (1-230) x US-10-063-515-79 (1-1475)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db 122 ATGGCTCTCTTGGCTCCCACTTGAGCTGCTACATCCTAGGCTTGGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTrpValGlyAlaSerIle 40
Db 182 ACCTGCTGGCCAGTGTGCTCCCAAGTGAAGAAAGTTCTTATGTCGGTGCAGCATT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 242 GTGACAGCAGTGGCTTCTTCCAGGGCTCTGATGGAATGTCCACACACAGCAGCAGGC 301
QY 61 IleThrGlnCysAspIleIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCAGGTGACATCTATAGCACCCCTTCTGGGCTGCGCCGTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIlysaSparGValAlaValAla 120
Db 422 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleProVal 140
Db 482 GGTGGAGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
Db 542 CAGGAGATCTTACAGGAGATCTTACAGGAGATCTTACAGGAGATCTTACAGGAGATCTTAC 601
QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GAGAGAGCTCTTACTTGGGCAATTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 661
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```
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCCCTGCTCATCTCCAGAGAAATCGCTCCAACTACATGATGCTTACAGGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIlyValLysSerGlu 220
Db 722 CAACTCTTTCACCAAGAGACTCTTCCAGGCTCTGATGATGATGATGATGATGATGATGATG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCAATTCTTCAAGCTTCAAGAGGATGATG 811

RESULT 14
US-10-063-512-79
; Sequence 79, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION: 2002-05-01
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-79

Alignment Scores:
Pred. No.: 2,43e-131 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-787-677a-3 (1-230) x US-10-063-512-79 (1-1475)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db 122 ATGGCTCTCTTGGCTCCCACTTGAGCTGCTACATCCTAGGCTTCTTGGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTrpValGlyAlaSerIle 40
Db 182 ACCTGCTGGCCAGTGTGCTCCCAAGTGAAGAAAGTTCTTATGTCGGTGCAGCATT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 242 GTGACAGCAGTGGCTTCTTCCAGGGCTCTGATGGAATGTCCACACACAGCAGCAGGC 301
QY 61 IleThrGlnCysAspIleIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCAGGTGACATCTATAGCACCCCTTCTGGGCTGCGCCGTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIlysaSparGValAlaValAla 120
Db 422 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 481
```

```

QY      121 G1YGIYValPhePheIleLeuGlyLeuLeuGlyPheIleProValAlaTPAanLeu 140
      |||
Db      482 GGTGGAGCTCTTTTCATCTTGAGGCTCTGGGATTCATCTGTGGCTGGAAATCTT 541
QY      141 H1G1YIleLeuArgAepPheTYrSerProLeuValProApsSerMetLysPheGluIle 160
      |||
Db      542 CATGGATCTTACGGGACTTCTACTCACACTGGTGGCTGACAGCAAGAAATTTGAATT 601
QY      161 G1YGIuAlaLeuTYrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
      |||
Db      602 GGAGAGGCTCTTACTGGGCAATATTTCTTCCCTGTTCCCTGATAGCTGGAAATCATC 661
QY      181 LeuCyPheSerCysserSerGlnArgApsApsSerLeuTYrTYrApsAlaTYrGlnAla 200
      |||
Db      662 CTCTGCTTTTCCCTGCTCATCCAGAGAAATCGCTCCAACTAAGATGCTTACCAAGCC 721
QY      201 G1nProLeuAlaThraArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
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Db      722 CAACCTTTGCCACAGAGGCTCTCCAGGCTTGTCACCTCCCAAGTCAAGATGAG 781
QY      221 PheAnSerTYrSerLeuThrGlyTYrVal 230
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Db      782 TTCATTCCTACAGCTGACGAGGTATGTG 811

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RESULT 15

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US-10-121-049-491
; Sequence 491, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlicsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gueney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33081C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; PRIORITY FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 550
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 491
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-121-049-491

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Alignment Scores:

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Pred. No.:      2,43e-131      Length:      1475
Score:          1174.00      Matches:      230
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              14          Gaps:      0

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US-09-787-677a-3 (1-230) x US-10-121-049-491 (1-1475)

```

QY      1 MetAlaSerLeuGlyLeuGlnLeuValGlyTYrIleLeuGlyLeuLeuGlyLeuLeuGly 20
      |||
Db      122 ATGGCCCTCTTGCCCTTCAAGCTTGTGGGCTTACATCCCAAGCTTTCTGGGCTTTTGGGC 181

```

```

QY      21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTYrValGlyAlaSerIle 40
      |||
Db      182 ACATGGATCTTCAATGCTGCTCCCACTGAGAAACAAAGTTCTTAATGCTGGTCCAGCATT 241
QY      41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
      |||
Db      242 GTGACAGCAATTTGGCTTCTCCAAAGGGCTCTGGATGGAATGTGCCACACACACAGCC 301
QY      61 IleThrGlnCysApsIleTYrSerThrLeuLeuGlyLeuProAlaApsIleGlnAlaAla 80
      |||
Db      302 ATCAACCAGATGACATCTATACACCTTCTGGGCTTGCCCTGATCATTCCAGGCTGCC 361
QY      81 G1AlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
      |||
Db      362 CAGGCCATGATGTGATGATCATCTGATGCAATCTCTCTGCTGCTGATTAATCTGTGGTG 421
QY      101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysApsArgValAlaValAla 120
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Db      422 GGCAATGATGACAGATCTTCTGCAAGAAATCCGAGCCAAAGACAGATGCGGTAGCA 481
QY      121 G1YGIYValPhePheIleLeuGlyLeuLeuGlyPheIleProValAlaTPAanLeu 140
      |||
Db      482 GGTGGAGCTCTTTTCATCTTGAGGCTCTGGGATTCATCTCTGTGGCTGGAAATCTT 541
QY      141 H1G1YIleLeuArgAepPheTYrSerProLeuValProApsSerMetLysPheGluIle 160
      |||
Db      542 CATGGATCTTACGGGACTTCTACTCACACTGGTGGCTGACAGCAAGAAATTTGAATT 601
QY      161 G1YGIuAlaLeuTYrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
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Db      602 GGAGAGGCTCTTACTGGGCAATATTTCTTCCCTGTTCCCTGATAGCTGGAAATCATC 661
QY      181 LeuCyPheSerCysserSerGlnArgApsApsSerLeuTYrTYrApsAlaTYrGlnAla 200
      |||
Db      662 CTCTGCTTTTCCCTGCTCATCCAGAGAAATCGCTCCAACTAAGATGCTTACCAAGCC 721
QY      201 G1nProLeuAlaThraArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
      |||
Db      722 CAACCTTTGCCACAGAGGCTCTCCAGGCTTGTCACCTCCCAAGTCAAGATGAG 781
QY      221 PheAnSerTYrSerLeuThrGlyTYrVal 230
      |||
Db      782 TTCATTCCTACAGCTGACGAGGTATGTG 811

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Search completed: December 20, 2004, 18:07:41
Job time : 550 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 13:31:01 ; Search time 3199 Seconds

(Without alignments)
2619.924 Million cell updates/sec

Title: US-09-787-677a-3

Perfect score: 1174

Sequence: 1 MASLGLVGLVILGLLGLG.....PGQPKVKESEFNSYSLGVV 230

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USPTO.spool/US09787677/runtat.20122004.132739.19443/app.query.fasta_1.391
-DB=EST -QFMT=fastap -SUFFIX=rest -NIMATCH=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62 -TRANS=human40.cdi -LIST=45
-NOCAI=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09787677@cgn2.1 1.3437@runtat.20122004.132739.19443 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	693	9	AY400251 Homo sapi
2	1137	96.0	693	9	AY400252 Pan trogl
3	1099	93.6	786	8	BZ215522 CH230-416
4	1096	93.4	693	9	AY400253 Mus muscu
5	1096	93.4	2829	3	AK004990 Mus muscu
6	1029.5	87.7	822	4	BG386074 602455248
7	1017	86.6	724	4	B1100253 602885716
8	1017	86.6	761	5	BP445902 BP445902
9	1014	86.4	727	4	B1101652 602887470

10	1002	85.3	680	2	BE304667	BE304667 601105783
11	1002	85.3	728	4	BG325755	BG325755 602424466
12	994	84.7	752	6	CB952500	CB952500 AGENCOURT
13	976.5	83.2	978	4	BG164062	BG164062 602341087
14	965	82.2	777	4	B1102100	B1102100 602887847
15	962.5	82.0	945	2	BE513091	BE513091 601171545
16	961	81.9	758	4	B1102679	B1102679 602888236
17	950	80.9	946	2	BF789255	BF789255 602105156
18	948	80.7	729	7	CN793010	CN793010 4127966 B
19	938	79.9	707	7	CK836649	CK836649 4061487 B
20	925.5	78.8	848	6	CA469366	CA469366 AGENCOURT
21	917	78.1	884	6	CA469620	CA469620 AGENCOURT
22	916.5	78.1	750	2	AM475316	AM475316 un64402.Y
23	909.5	77.5	706	4	B1148156	B1148156 602912333
24	908	77.3	685	7	CK975368	CK975368 4106482 B
25	903	76.9	818	6	CA469360	CA469360 AGENCOURT
26	900.5	76.7	804	2	BF784189	BF784189 602108052
27	895	76.2	666	9	CE239984	CE239984 L19T-S88-
28	880	75.0	704	4	B1330754	B1330754 6029882419
29	875.5	74.6	754	4	BG972599	BG972599 602841188
30	869	74.0	648	7	CN788131	CN788131 4122426 B
31	868	73.9	836	6	CA492032	CA492032 AGENCOURT
32	865	73.7	650	7	CR546700	CR546700 DXFZP470L
33	865	73.7	652	7	CR628947	CR628947 DXFZP469L
34	862	73.4	1114	2	CK031415	CK031415 AGENCOURT
35	861	73.3	774	4	BF789836	BF789836 602105395
36	859	73.2	787	2	BF781962	BF781962 602106220
37	854	72.7	673	1	A1746723	A1746723 u106109.Y
38	843	71.8	643	4	BG328625	BG328625 602427889
39	838	71.4	678	5	BP138412	BP138412 BP138412
40	832	70.9	659	1	A1789490	A1789490 u99h03.Y
41	823	70.1	674	4	B1102491	B1102491 602889685
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Homo sapiens CLDN2 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION AY400251
VERSION AY400251.1 GI:39756240
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
1 (bases 1 to 693)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE
Infering nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL
PUBMED 14671302
2 (bases 1 to 693)

REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE
Direct Submission

JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
source location/Qualifiers
1..693

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    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
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    /gene="CLDN2"
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Score:	1174.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
Length:	693
Matches:	230
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-787-677A-3 (1-230) X AY400251 (1-693)

QY	1	MeAlSerLeuGlYleuGlInLeuValGlyTrIleLeuGlYleuGlYleuGlY	20
Db	1	ATGGCTCTCTTG6CCTCCAACTGTGGGCTTCACTTGA6GCTTTCGG6GCTTTT66G	60
QY	21	ThrLeuValAlaMetLeuLeuProSerTrpYsthrSerSerTrValGAlaSerIle	40
Db	61	ACACTGGTGGCATGTGCTGCCACGCTGGAAAACAATTCTTATGTGGGCGCAGATT	120
QY	41	ValThrAlaValGlyPheSerLeuGlyLeuTrpMetGluCysAlaThrHisSerThrGly	60
Db	121	GTGACGAGCAAGTGGCTTCTCCAAAGGGCCTCTGATGAGATGTGCACACACAGCAGGC	180
QY	61	IleThrGlnCysAspIleTyrSerThrThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla	80
Db	181	ATACCCAGAGTGACACTTATAGACACCCCTTCTGGGCGCTGGCGGTGATCTCAGAGCTGCC	240

QY	8	GLA1MeMeValThrSerSerLaiIleSerSerLauAlaCysIleIleSerVal	100
Db	241	CAGGCATATGGTGCATCCAGTCGATCTCTCTCGCCTGCATTATCTCTGGTG	3000
QY	101	GLYMeIarGCSrThrValPheCysgInguSerIarGalAlaYbaPdaValAlaValAla	120
Db	301	GGCATAGATGCACACTCTTCTGCCAGGATATCCGACGAAGAAGACAGTGCGCGTGGCA	360

QY	122	GLVGLVVal.PhepheheleuengljygljleuengljyPheileproValAlaAlaPheleu	140
Db	361	GGGGAGCTCTTTTCACTCTTGGAGGCCCTCGGGATTCATCTCGTGGCTGGAACTTT	420
QY	141	HisGLYIleleuArgAspPheTyrsrProleuValProAspSerMetLysPheGluIle	160
Db	421	CAAGGAGATCCTACGGGACTTCTACACCACTGGGGCTGACAGCATGATAAATTTTGAATTT	480

Qy	Db
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181	181
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541	600

Qy	Dy
201	601
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Leu	CAAGAGAGCT
Thr	CTCCAAAGCGCTGGT
Arg	CTCAACTCCCAAA
Ser	GAAGTGAAG
Pro	
Ala	
Gly	
Val	
Ser	
Glu	
220	660
221	
Phe	
Asn	
Ser	
Thr	
Leu	
Gly	
Val	
230	
661	
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ACAGCTGAC	
AGGAGTATG	
690	

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LOCUS	AY400252				
DEFINITION	Pan troglodytes CLDN2 gene, VIRTUAL TRANSCRIPT, partial sequence,				
ACCESSION	AY400252				
VERSION	AY400252.1	GI:39756241			

KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes

CLADANISM
 FEAR, C. L. G. 1963
 Eukaryotes; Metazoa; Chordata; Craniata; Euteleostomi
 Mammalia; Eutheria; Primates; Carnivori; Homiidae; Pan.
 1 (bases 1 to 693)
 REFERENCE
 AUTHORS
 Clark, A. G., Gnanowski, S., Nielson, R., Thomas, P., Kojima, A.,

TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL	PUBMED	REFERENCE	AUTHORS
Science 302 (5652), 1960-1963 (2003)	14671302	2 (bases 1 to 693)	Clark, A.G., Gjanowski, S., Nielson, R

Todd, M.A., Tanenbaum, J.W., Civerio, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.

TITLE Direct Subduction
JOURNAL Submitted (16-NOV-2003) *Celera Genomics*, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

Source

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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>693
/gene="UCP2"

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ORIGIN

Alignment Scores:

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Percent Similarity:	96.52%	Conservative:	0
Best Local Similarity:	96.52%	Mismatches:	8
Query Match:	96.00%	Indels:	0
DB:	9	Gaps:	0

US-09-787-677A-3 (1-230) X AY400252 (1-693)

Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGly 2
Db 1 ATGGCCCTCTCTGGCCCTCCAACTTGTGGNNNNNAATNTATNCCNNNGGGCTTTTGGCC 6
Qy 21 ThrIleValAlaMetLeuLeuProSerTrpIleThrSerSerTyrValGlyAlaSerIle 4

Dd		61	ACNNGTGGTCGATGCTGCCTCCAGCTGGAAAAACAATTCTTAACGTGGTGCAGCAATT	1
Oy	41	ValThrLlaValAlglyPheSerIysGlyLeuTrpMetGluCysAlaThrHisSerThnGly	6	
Dd	121	GTCACACAGAATTGGCTCTCCAAAGGCGCTTGATGTGAATGTGCCACACACACAGCAGC	1	
Oy	61	IleThrGlnCysAspIleIyrSerThrIleuLeuGlyLeuProLaaAspIleGlnAlaA	8	

Accession	Protein	Length
Db	181 ATCACCCAGGTGATGACATCTTAGACACCCCTTGGGGCTGGCCGCTGACATCCAGGGCTGC	20
Oy	81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal	1
Db	241 CAGGCATGATGGTGACATCCAGTGCATCTCTCCCTGGCCGTGCATTAATCTCTGGTGTG	3
Oy	101 GlyMetArgCysThrValPheCysGlnGlnSerAlaAlaLysAspArgValAlaValAla	1

[illegible]

Db	421	CATGGAGTCTCAGGACCTTACTCAACCATGGTGCGCTGCACACATGAATTTCGAGATT	480
Oy	161	GlyGUAlALeuTYrLEUGLYlleIleSerSerLeuPheSerLeuIleAlAGLYlleIle	180
Db	481	GGAGAGGCTCTTTACTTGGGACATTAATTTCTTCCTCGTTCTCCGTGATAGCTGAATCATC	540
Oy	181	LeuYasPheSerCySeSerSerGLnArgAsnArgSerLanTYrTyraAPAlATYcGlAlA	200
Db	541	CTTGCGCTTTTCTCTCATCTCCAGAAATGCTCCAACATACTACGATCGCTACCAGGCC	600
Oy	201	GlnProLeuAlATInrArgSerSerProArgProGlyGlnProPolySValysSerGlu	220
Db	601	CAACCTCTTGCCACAAGAGCTCTCCAGAGCGCTGCTCACTCTCCCAANGTCAAGAGTGAG	660
Oy	221	PheAnsErTYrSerLeuThnGYTYrVal	230
Db	661	TTCATTCTCTACAGCTGACAGGATGTG	690
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BZ215522			
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VERSION	CH230-416N16		genomic survey sequence.
KEYWORDS	BZ215522		
SOURCE	BZ215522.1	GI:23873880	
ORGANISM	GSS.		
REFERENCE	Rattus norvegicus (Norway rat)		
AUTHORS	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 786) Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Frazer,C.M. Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished (1999) Other GSSs: CH230-416N16.TU Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Genomes are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pletier de Jong (pjejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html Plate: 416 row: N column: 16 Seq primer: T7 Class: BAC ends.		
JOURNAL COMMENT			
TITLE			
FEATURES			
Source			
ORIGIN			
Alignment Scores:			
Pred. No.:	1,04e-113	Length:	786
Score:	1099.00	Matches:	211

US-09-787-677A-3 (1-230) x B215522 (1-786)	Best Local Similarity: 96.09%	Conservative: 10
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		Gaps: 0
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Db	59 ATGGCCCTCCCTGGAGCGTCCAACTGCTGGGCTACATCTCAGGCTTTGGGGCTATTAGGC	118
OY	21 ThiruVal1aMetLeuLeuLeuProSerTyrThrSerSerTyrValGlyValSer1le	40
Db	119 ACATCGATTGCCATGCTGCTCCCAACTGGGCGAACAAGTTCTTATGTTGGGCCAGCATTT	178
OY	41 Val1Thru1aValGlyPheSerLyGlyLeuTyrPheGlyCysValarHisSerThryGly	60
Db	179 GTGACGGGGGTGGCTTTTCCAAAGGCGCTTGANTGGAGTGTGGACCCACAGCATGGC	238
OY	61 IleThrGlyCysAsp1IerYrSerThrLeuLeuGlyLeuPro1aAsp1leGln1a1a	80
Db	239 ATCCACCAAGTGTGATCTTACAGTACTTTTATAGACTTCTGTGTGACATCCAGCTGCGC	298
OY	81 Gln1aMetMetVal1ThrSerSer1a1leSerSerLeu1aCys1le1leSerValVal	100
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OY	101 GlyMetArGySthrrValPheCyGlnGlnuSerArg1a1a1aAspArgVal1aVal1a	120
Db	359 GGCATGAGATCCACAGTCTTCTGCCAGGAATCTGAGCTAAGACAGAGTGGCTGTATGTG	418
OY	121 GlyGlyValPhePhe1leLeuGlyGlyLeuLeuGlyPhe1leProVal1a1TyrPasnLeu	140
Db	419 GGTGAGAGCTTTTTCATCTTGGTGGTATCCTGGGTATTTATCCAGTGTCTGGCATCTT	478
OY	141 HisGly1leLeuArgAspPheTyrSerProLeuValProAspSerMetLyPheGln1le	160
Db	479 CACGGCATCTCCGGAGCTTCTACTCATCCACTGTGCTCCGTGACACATGMAATTTGGATT	538
OY	161 GlyGln1a1aLeuTyrLeuGly1le1leSerSerLeuPheSerLeu1le1aGly1le1le	180
Db	539 GGAAAGACTCTGTACTTGGGAATATTTACAGCGCTTTTCTCTTGTAAGCTGGAGTCAATC	598
OY	181 LeuCySphSerCySserSerGlnArgAsnArgSerAsnTyrTyrAsp1a1aTyrGln1a	200
Db	599 CTGCGCTTTCTCTCTCACTCAGGAAATGTATCAACATCTATGATGGCTTACAGGCC	658
OY	201 GlnProLeu1a1aThrArgSerSerProArgProGlyGlnProPolYVal1a1aSerGly	220
Db	659 CAGCGCTTGGCCATGAGAGCTCTCCCAAGATCTGCTCAACAGCCCAAGCCMAAGTGAAG	718
OY	221 PheAsnSerTyrSerLeuThrGlyTyrVal 230	
Db	719 TTCAACTCATACAGCTGAGCTGGGTATGTG 748	
RESULT 4		
AY400253	693 bp	DNA linear
LOCUS		
DEFINITION	Mus musculus CLDN2 gene, VIRUTAL TRANSCRIPT, partial sequence,	
ACCESSION	AY400253	
VERSION	AY400253.1	
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 693)	
REFERENCE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.U., Adams,M.D. and Cargill,M.	
AUTHORS		
TITLE	Interfering nonneutral evolution from human-chimp-mouse orthologous	

gene trios
 Science 302 (5652), 1960-1963 (2003)
 14673302
 2 (bases 1 to 693)
 Clark, A.G., Ghanowaki, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
 Parlier, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 COMMENT location/Qualifiers
 FEATURES
 source
 1. 693
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 <1..>693
 /gene="CLDN2"
 /locus_tag="HGM0495"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,91e-113 Length: 693
 Score: 1096.00 Matches: 210
 Percent Similarity: 96.09% Conservative: 11
 Best Local Similarity: 91.30% Mismatches: 9
 Query Match: 93.36% Indels: 0
 Gaps: 0
 US-09-787-677a-3 (1-230) x AY400253 (1-693)
 QY 1 MetTlaSerLeuGlyLeuGlnLeuValGlyTrrTleuGlyLeuGlyLeuGly 20
 Db 1 ATGGCCCTCCCTGGCGTCACTGAGTGGCTACATCCAGGCTTTGGGCGTGTAGGC 60
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrrPlyrThrSerSerTrrValAlaSerTle 40
 Db 61 ACATCCATTGGCATGCTGCTCCCACTGGGAACGAGATTCCTTGTGGCCAGCATT 120
 QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTrrPmetGlyCysAlaThrHisSerTrrGly 60
 Db 121 GTGACGGCGGTGGCTTTTCCAGAGGCGCTTGATGAGTGTGCACACACAGCAGGC 180
 QY 121 IleThrGlnCysAspTrrTrrSerTrrLeuGlyLeuProAlaAspTleGlnAlaAla 80
 Db 61 IleThrGlnCysAspTrrTrrSerTrrLeuGlyLeuProAlaAspTleGlnAlaAla 80
 QY 181 ATCCACCGATGCGATATCTACAGTACCTTTAGACTTCTGTGACATCCAGGCTGCC 240
 Db 81 GlnAlaMetMetValTrrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 QY 241 CAGGCCATGATGTGAGCTCCAGTCCAGTATGCTCGCTGCTGTATTTATCTCTGTGTG 300
 Db 101 GlyMetArgCysThrValPheCysGlnGlnSerAlaValAlaValAlaValAla 120
 QY 301 GGCAATGAGATGCACCGTGTCTGTCAGAGATTCTCGAGTAAAGACAGAGTGGTGTAGTG 360
 Db 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrrPasnLeu 140
 QY 361 GGTCGAGATCTTTTTCATCTCTGGGCGCATCTCGGCTTTTACCCAGATGCTTGAATCTT 420
 Db 141 HisGlyIleLeuAlaGAspPheTrrSerSerProLeuValProAspSerMetLeuPheGlnIle 160
 QY 421 CATGGCATCTCTCGGACTTCTACTCCGCGCTGTTCTTGACACAGATGAATTTGAGATT 480
 Db 161 GlyGlnAlaLeuTrrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 QY 481 GGAAGAGCTCTGTACTTGGGATCATCTCAGCCGTGTTTCTTGTGTAGCGGAGTATC 540
 Db 181 LeuCySerSerCysSerSerGlnArgAsnArgSerAntTrrTrrAspAlaTrrGlnAla 200
 QY 541 CTTTGTCTTTCTCTGCGCCCGAGGGCGATGTACCAACTACTATGATGCTTACAGGCC 600

QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPlyValysSerGln 220
 Db 601 CAGCCTTTCCTCCACTGAGACTCTCCCAAGATGTGCTCAACAGCCCAAGCAAGAGTGA 660
 QY 221 PheAsnSerTrrSerLeuThrGlyTrrVal 230
 Db 661 TTCACATCATACAGCTGACTGGGTATGTG 690
 RESULT 5
 AK004990
 LOCUS
 DEFINITION
 Mus musculus adult male liver cDNA, RIKEN full-length enriched
 library, clone:1300019606 product:claudin 2, full insert sequence.
 ACCESSION
 AK004990
 VERSION
 AK004990.1 GI:12836594
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitasumi, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujisake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Machiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 2829)
 Adachi, T., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
 Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
 Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hizumoto, K.,
 Hirooka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
 Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Maezuyama, T., Miyazaki, A., Nishi, K.,
 Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
 Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
 Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y.,
 Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
 Tejima, Y., Toyama, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
 Yoshino, M., Yuramatsu, M. and Hayashizaki, Y.
 Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of

Qy 143 eLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIleGlyGluVal 163
 Db 455 CTTTCGGAGCTTTACTTCGCCGCTGTTCTTGACAGCATGAATTCAGATTGGAGAGGC 514
 Qy 163 aLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleIleGlyIleIleLeuGlySph 183
 Db 515 TCTGTACTTGGGATCATCTCAGCCCTGTTTCTTTGTGTAGCCGAGTATCTTGTGCTT 574
 Qy 183 eSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnIleGln-Prol 203
 Db 575 TTCTCTCTCCGCCCGAGGCAATGTACCAACTACTATGATGCTACCGAGCCAGACTTC 634
 Qy 203 eulAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGluPheAsn 223
 Db 635 TTGCCCTAGAGACTCTCCAGATCTGCTCTCAACAGCCCAAGCCAGAGTTCACACT 694
 Qy 223 eTyrSerLeuThrGlyTyrVal 230
 Db 695 CATACAGCTGACTGGGTATGTG 717

RESULT 8
 BP445902 761 bp mRNA linear EST 30-DEC-2003
 LOCUS BP445902 full-length enriched swine cDNA library, adult liver Sus
 DEFINITION scrofa cDNA clone LVR010047F07 5', mRNA sequence.
 ACCESSION BP445902 GI:40435969
 VERSION BP445902.1
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 1 (bases 1 to 761)
 Uenishi,H., Egyuchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
 Okumura,N., Hamasima,N. and Awata,T.
 PEDS (Pig EST Data Explorer): construction of a database for ESTs
 derived from porcine full-length cDNA libraries
 Nucleic Acids Res. 32 (1), D484-D488 (2004)
 CONTACT: Hirohide Uenishi
 Animal Genome Laboratory, Genome Research Department
 National Institute of Agrobiological Sciences
 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: +81-29-838-8627
 Fax: +81-29-838-8627
 Email: huenishi@affrc.go.jp
 EST project with full-length enriched cDNA libraries carried out in
 Animal Genome Research Program (Japan) by National Institute of
 Agrobiological Sciences and STAFF-Institute
 Single pass sequencing of clones derived from oligo-capped cDNA
 library
 Vector sequences were eliminated by RepeatMasker version 2002/07/13
 and crossmatch version 0.990319
 Low quality bases were trimmed based on the quality values.
 Location/Qualifiers
 1..761
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="LVR010047F07"
 /tissue_type="liver"
 /dev_stage="adult"
 /clone_lib="full-length enriched swine cDNA library, adult
 liver"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,95e-104 Length: 761
 Score: 1017.00 Matches: 199
 Percent Similarity: 97.60% Conservative: 4
 Best Local Similarity: 95.67% Mismatches: 5
 Query Match: 86.63% Indels: 0
 DB: 5 Gaps: 0

US-09-787-677a-3 (1-230) x BP445902 (1-761)
 Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGly 20
 Db 138 ATGGCTCTCTCCGCTCCCAACTTGTAGGCTATCATCTTGGGCTTCTGGGC 197
 Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValGlyAlaSerIle 40
 Db 198 ACCCTGTGGCCATGCTGCTCCACAGTGGCAGACAGATTCTTAAGTGGGCGAGCATC 257
 Qy 41 ValThrAlaValGlyPheSerLysGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
 Db 258 GTACCGGAGTGGCTCTTCTCAAGGCTCTGTGATGAGTGTCCAGCAGACACTGGC 317
 Qy 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 Db 318 ATCACCAGTGTGACATCTACAGACACAGCTGGGCTGCTGCTGACATCCAGCTGCC 377
 Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 378 CAGGCCATGATGTGATGACATCTAGCCCATCTCTCTGTGCTGTATCATCACCGTGTG 437
 Qy 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
 Db 438 GGCATCGGATGGACCGCTCTTCTCCAGAACTCTCGGCCAAGACAGAGTGGCGTGTG 497
 Qy 121 GlyIleValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrPheLeu 140
 Db 498 GGTGAGTCTTCTTCTCTTGGAGGCTCTTGGCTTCATCCCTGTGCGTGAATCTT 557
 Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 Db 558 CATGGATCTCTGGGACCTTACTCTCCCTGCTGCTGACAGCAAGAAATTTGAGATC 617
 Qy 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleIleGlyIleIle 180
 Db 618 GAGAGGCTCTCTACTTGGGCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 677
 Qy 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 678 CTCTGCTTTTCCGCCCACTGCAAGAAATCGCTCAACTACATGATGCTATCAGGCC 737
 Qy 201 GlnProLeuAlaThrArgSerSer 208
 Db 738 CAGCCCTCGCCACCCGAGCTCT 761

RESULT 9
 B1101652 727 bp mRNA linear EST 26-JUN-2001
 LOCUS B1101652
 DEFINITION 602867470F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5042825
 5', mRNA sequence.
 ACCESSION B1101652
 VERSION B1101652.1 GI:14552545
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 727)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1AM1117 row: k column: 18
 High quality sequence stop: 722.

FEATURES
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Location/Qualifiers
1..727
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5042825"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NCI CGAP Kid14"
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP library." |"

ORIGIN
Alignment Scores:
Pred. No.: 4.01e-104 Length: 727
Score: 1014.00 Matches: 194
Percent Similarity: 97.62% Conservative: 11
Best Local Similarity: 92.38% Mismatches: 5
Query Match: 86.37% Indels: 0
DB: Gaps: 0

US-09-787-677a-3 (1-230) x B1101652 (1-727)

Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 90 ATGGCTCCCTGGCTGCACTGGTGCGTCAATCCAGGCTTTGGGCTGTAGGC 149
Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
Db 150 ACATCCATTCGCATGCTGCTCCCACTGGCGAAGCGATTCCTATGTTGGTCCAGCAT 209
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaIleThrHisSerThrGly 60
Db 210 GTGACGGCGGTGGCTTTCCAGGGCTCTGAGTGTGGACACACACAGCAGCC 269
Qy 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
Db 270 ATCACCAGGCGATCTACAGTACGATCCCTTTAGACTCTGCTGACATCAGGCTGCC 329
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 330 CAGGCCATGATGGAGTGCAGTGCAGTACATGCTCGGCTTGATATCTCTGTGTG 389
Qy 101 GlyMetArgCysThrValPheCysGlnIleSerIleGlnAlaValAlaValAla 120
Db 390 GGCATGATGACACCGTGTCTGCGCAGATTCCTGAGCTAAGACAGAGTGTAGTG 449
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaIleProVal 140
Db 450 GGTGGAGTCTTTTCACTCTGTGGCATCTGGGCTTTATCCAGTTCCTGGAACTTT 509
Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlePheGlu 160
Db 510 CATGGATCTCTGGGACTTCTACTCGCGCTGTCTGACACATGAATTTGAGATT 569
Qy 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
Db 570 GGAAGAGCTGTGATCTGGGATCATCTCAAGCTGTTTCTTGTAAGCGGAGTATC 629
Qy 181 LeuCysPheSerCysSerSerGlnArgAspArgSerAntTyrIleAspAlaTyrGln 200
Db 630 CTTTGTCTTCTCTGCGCCCAAGGCAATGATCACTAATGATGCTACAGGCC 689
Qy 201 GlnProLeuAlaThrArgSerSerProArg 210
Db 690 CAGGCTCTTGCCACTAGAGCTCTCCAAGA 719

RESULT 10
BE304667
LOCUS
DEFINITION 601105783F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988309 5'

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
mRNA sequence.
BE304667
BE304667.1 GI:9176036
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Mammalia; Eukarya; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eukarya; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 680)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ARCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
plate: LNCM77 row: f column: 22
High quality sequence start: 27
High quality sequence stop: 680.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2988309"
/issue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MGC 15"
/note="Organ: colon; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT printing. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN
Alignment Scores:
Pred. No.: 8.36e-103 Length: 680
Score: 1002.00 Matches: 195
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.35% Indels: 0
DB: Gaps: 0

US-09-787-677a-3 (1-230) x BE304667 (1-680)

Qy 36 ValGlyAlaSerIleValIleThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAla 55
Db 38 GTCGTCACGACATTTGACAGCAGTGTCTTCCAGGCGCTCTGATGATGTGCC 97
Qy 56 ThrHisSerThrGlyIleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAla 75
Db 98 ACACACGACACAGGACATCCAGTGTGACATCTAATGACCCCTTGTGGCGCTGCCGCT 157
Qy 76 AspIleGlnAlaIleGlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCys 95
Db 158 GACATCAGGCTGCCCGGCGCATGATGATGATCATCCAGTCCATCTCTCTGGCTGC 217
Qy 218 ATTATCTCTGTGGGCGCATGATGATGATGATGATGATGATGATGATGATGATGAT 277
Db 218 ATTATCTCTGTGGGCGCATGATGATGATGATGATGATGATGATGATGATGATGAT 277
Qy 116 ArgValAlaValAlaGlyGlyValPhePheIleLeuGlyIleLeuGlyPheIlePro 135
Db 278 AGAGTGGCGGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 337
Qy 136 ValAlaIleProLeuHisGlyIleLeuArgAspPheTyrSerProLeuValProAspSer 155


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Db      338 GTTGCTGGAATCTTCATGGAGATCTTCAGGACCTTCTACTCACCACCTGGTGGCTGACAGC 397
Qy      156 MetLysPheGluIleGlyGluAlaLeuTyrlleuGlyIleIleSerSerLeuPheSerLeu 175
Db      398 ATGAATTTGAGATTGGAGAGGCTCTTACTTGGGATTAATTTCTTCCTGTTCTCCCTG 457
Qy      176 IleAlGlyIleIleLeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrlle 195
Db      458 ATAGCTGGAATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 517
Qy      196 AAPAlATyrlGlnIleGlnProLeuAlaThrArgSerSerProArgProGlyGlnProPro 215
Db      518 GATGCTACCAAGCCCAAGCTCTTGGCCCAAGAGCTCTCCAGAGCTGGTCAACTCTCC 577
Qy      216 LysValIleSerGlnPheAsnSerTyrlSerLeuThrGlyTyrlVal 230
Db      578 AAGTCAGAGTGAGTTCAATTCCTACAGCCTGACAGGTATGTG 622

```

```

RESULT 11
LOCUS    BG325755          728 bp      mRNA          linear      EST 27-FEB-2001
DEFINITION
602424466F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4562273 5',
mRNA sequence.
ACCESSION
BG325755
VERSION  BG325755.1  GI:13132179
KEYWORDS
EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

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REFERENCE
1 (bases 1 to 728)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabs-remail.nih.gov
          Tissue Procurement: DCTD/DTF

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CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM1274 row: d column: 18
High quality sequence stop: 708.
location/Qualifiers

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FEATURES
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1..728
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4562273"
/risue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_14"

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/note="Organ: kidney; Vector: pOTB7, Site_1: XhoI, Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA Synthesis Kit
(Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

Alignment Scores:

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Pred. No.: 9.2e-103      Length: 728
Score: 1002.00      Matches: 218
Percent Similarity: 95.22%      Conservative: 1
Best Local Similarity: 94.78%      Mismatches: 10
Query Match: 85.35%      Indels: 6
DB: 4      Gaps: 1

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US-09-787-677a-3 (1-230) x BG325755 (1-728)

```

Qy      1 MetAlSerLeuGlyLeuGlnLeuValGlyTyrlleuGlyLeuLeuGlyLeuGly 20
Db      30 ATGGCTCTCTTGGCTCCCAACTGTGGGCTACATCTGAGCCTTCTGGGGCT- TTGGGC 88
Qy      21 ThrLeuValAlaMetLeuLeuProSerTyrlPheThrSerSerTyrlValGlyAlaSerIle 40
Db      89 ACACGTGTCCACATGCTGCTCCACCTGGAGAAAACAAAGTTCTTAGTGGGTGCAGCATT 148
Qy      41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGluCysAlaThrHisSerTrngly 60
Db      149 GTGACAGCAAGTTGGCTTCTCCAAAGGCTCTGGATGGAATGTCCACACACACAGGC 208
Qy      61 IleThrGlnCysAspIleTyrlSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db      209 ATCACCAGATGATCATCTATACACCTCTGAGGCTGCTGCCCTCAATCCAGGCTGCC 268
Qy      81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db      269 CAGGCCATGATGATGATGATCAGTGCATCTCTCCCTGGCTGCAATATCTGTGGTG 328
Qy      101 GlyMetArgSerThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaAla 120
Db      329 GGCATGAGATGACACAGCTCTTCTCCAGGAATCCCGAACACAGAGTGGGATGCA 388
Qy      121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTrpAsnLeu 140
Db      389 GGTGTGATCTTTTTCATCTCTGAGGCTCTGGAATTCATTCCTGTGCTGCAATCTT 448
Qy      141 HisGlyIleLeuArgAspPheTyrlSerProLeuValProAspSerMetLysPheGluIle 160
Db      449 CATGGATCTCTACGGAGCTTACTCACTGATGCTGACAGCAAGAAATTTAGATT 508
Qy      161 GlyIleAlaLeuTyrlleuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db      509 GAGAGGCTCTTACTTGGGCAATATTTCTCTCTGCTTCTGATGATGATATATC 568
Qy      181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrlTyrlAspAlaTyrlGlnAla 200
Db      569 CTCGTCTTTCCTGCTCATCTCCAGAAATCGCTCAACTACATGATGATGATGATG 628
Qy      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db      629 AACTCT--TGACCAAGAGCTCTCCAGGCT-GGTCACT-CCCAAGTCAGAGTGTAG 683
Qy      221 PheAsnSerTyrlSerLeuThrGlyTyrlVal 230
Db      684 TC-ATTTCCTACAG-CTGACAGGATATGTG 711

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RESULT 12
LOCUS    CB952500          752 bp      mRNA          linear      EST 29-APR-2003
DEFINITION
AGENCOCURT 13692613 NIH_MGC_176 Mus musculus cDNA clone
IMAGE:30303557 5', mRNA sequence.
ACCESSION
CB952500
VERSION  CB952500.1  GI:30208619
KEYWORDS
EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE
1 (bases 1 to 752)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabs-remail.nih.gov
          Tissue Procurement: Dr. Michael Brownstein
          cDNA Library Preparation: Michael Brownstein Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be

```

found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: NDCM74 row: e column: 06
 High quality sequence stop: 586.
 Location/Qualifiers

FEATURES

Source

1. 752
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:30303557"
 /lab_host="DH10B (TI-phage-resistant)"
 /clone_id="NIH_MGC_176"
 /note="Organ: kidney; Vector: pDNR-LIB; Site 1: SfiI (ggcgatcgccgc); Site 2: SfiI (ggcgatcgccgc); cDNA made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
 5'-AGCAGATGATCAACGACAGATGAGCCATTCAGCCGCG-3' and
 5'-ATTCTAGAGCCGAGCGGCGGACATG-3' (30)NM-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5 kb size fraction. Library created in the laboratory of M. Brownstein (NIH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 7.76e-102 Length: 752
 Score: 994.00 Matches: 190
 Percent Similarity: 97.57% Conservative: 11
 Best Local Similarity: 92.23% Mismatches: 5
 Query Match: 84.67% Indels: 0
 DB: 6 Gaps: 0

US-09-787-677a-3 (1-230) x CB952500 (1-752)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTlleLeuGlyLeuLeuGly 20
 Db 108 ATGGCCCTCCCTGGCTGCAACTGCTGGGCTACATCTCAGGCTTTGGGCTGTAGGC 167
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysTrpSerSerTyrValGlyAlaSerTlle 40
 Db 168 ACATCCATGTCATGCTGCTTCCCACTGCGAAGCGAGTTCTTATGTTGGCCAGCATTT 227
 QY 41 ValThrAlaValGlyPheSerTlleGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
 Db 228 GTGACGGCGGTGGCTTTCCAGAGGCTCTCGATGAGTGTGGACACACAGCAGCGC 287
 QY 61 IleThrGlnCysAspTlleTyrSerThrLeuGlyLeuProAlaAspTlleGlnAla 80
 Db 288 ATCACCAGTGCATCTACATCAGTACCTTTTACGACTTCTGCTGACATCCAGGCTGCC 347
 QY 81 GlnAlaMetMetValTrpSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 348 CAGGCCATGATGTCAGATGTCAGATGATGTCCTGCTGCTGCTGCTGCTGCTGCTG 407
 QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
 Db 408 GGCATGAGATGACACGATGCTTCCAGAGATCTCGAGCTAAGACAGAGTGGCTGTG 467
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
 Db 468 GGTGGAGTCTTTTTCATCTTGTGGGCAATCTGCGCTTATCCAGATTTGGAATCTT 527
 QY 141 HisGlyIleLeuAlaGlyAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
 Db 528 CATGGCATCTTCCGAGCTTCTACTCGCGCTGTGTCTCTGACAGCAAGAAATTTGAATT 587
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 Db 588 GAGAGAGCTCTGTACTTGGGATCATCTCAGCCCTGTTTCTTTGGTAGCGGAGTCATC 647
 QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerArgTyrTyrAspAlaTyrGlnAla 200
 Db 648 CTTTGTCTTCTCTGCGCCCAAGGCAATGTGATCAAACTACTATGATGGCTACAGGCC 707

QY 201 GlnProLeuAlaThrArg 206
 Db 708 CAGCCTCTTCCCACTAG 725

RESULT 13

BG164062 978 bp mRNA linear EST 06-FEB-2001
 LOCUS 602341087F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4449212 5',
 DEFINITION mRNA sequence.

ACCESSION BG164062.1 GI:12670765

VERSION BG164062.1 GI:12670765

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 978)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@ds-femail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM10232 row: m column: 21
 High quality sequence stop: 689.
 Location/Qualifiers

FEATURES

Source

1. 978
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4449212"
 /tissue="IMAG:4449212"
 /lab_host="DH10B (phage-resistant)"

/clone_id="NIH_MGC_89"
 /note="Organ: kidney; Vector: pCMV-Sport6; Site 1: NotI,
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1.08e-99 Length: 978
 Score: 976.50 Matches: 218
 Percent Similarity: 93.99% Conservative: 9
 Best Local Similarity: 93.56% Mismatches: 9
 Query Match: 83.18% Indels: 1
 DB: 4 Gaps: 1

US-09-787-677a-3 (1-230) x BG164062 (1-978)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTlleLeuGlyLeuLeuGly 20
 Db 25 ATGGCCCTCTTGGCTGCAACTGCTGGGCTACATCTCAGGCTTTGGGCT-TTGGGC 83
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysTrpSerSerTyrValGlyAlaSerTlle 40
 Db 84 ACATGATGTCATGCTGCTTCCCACTGCGAAGCGAGTTCTTATGTTGGCCAGCATTT 143
 QY 41 ValThrAlaValGlyPheSerTlleGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
 Db 144 GTGACAGCATTTGGCTTCTCAGAGGCTCTGATGAGTGTGGACACACAGCAGCGC 203
 QY 61 IleThrGlnCysAspTlleTyrSerThrLeuGlyLeuProAlaAspTlleGlnAla 80
 Db 204 ATCACCAGTGTACATCTATGACACCTTCTGCGGCTGCGCTGACATCCAGGCTGCC 263

FEATURES	source
1. .777	
Location/Qualifiers	
High quality sequence stop: 749.	
Plate: L14M1118 row: m column: 12	
http://image.llnl.gov	
found through the I.M.A.G.E. Consortium/LLNL at:	
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
Clone distribution: MGC clone distribution information can be	
contacted through the I.M.A.G.E. Consortium/LLNL at:	
Unpublished (1999)	
National Institutes of Health, Mammalian Gene Collection (MGC)	
NIH-MGC http://mgc.nci.nih.gov/.	
1 (bases 1 to 777)	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mus musculus (house mouse)	
EST.	
Accession	
Version	
Keywords	
Source	
Organism	
Comment	
Journal	
Title	
Authors	
Reference	
LOCUS	
DEFINITION	
5', mRNA sequence.	
Accession	
Version	
Keywords	
Source	
Organism	
Comment	
Journal	
Title	
Authors	
Reference	
LOCUS	
DEFINITION	
5', mRNA sequence.	
Accession	
Version	
Keywords	
Source	
Organism	
Comment	
Journal	
Title	
Authors	
Reference	
LOCUS	
DEFINITION	
5', mRNA sequence.	
Accession	
Version	
Keywords	
Source	
Organism	
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Journal	
Title	
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Accession	
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Accession	
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Accession	
Version	
Keywords	
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Comment	
Journal	
Title	
Authors	
Reference	
LOCUS	
DEFINITION	
5', mRNA sequence.	

ORIGIN	Alignment Scores:	1.57e-98	Length:	777
Pred. No.:	Score:	965.00	Matches:	185
Percent Similarity:		96.60%	Conservative:	14
Best Local Similarity:		89.81%	Mismatches:	7
Query Match:		82.20%	Indels:	0
DB:		4	Gaps:	0
US-09-787-677A-3 (1-230) x B1102100 (1-777)				
QY	1	MetaIaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly	20	
DB	153	ATGGCTCTCCCTGGCGATTCAACTGAGGCTCACTCAAGCCCTTTGGGGCTTTAGGC	212	
QY	21	ThirleuValAlaMetLeuLeuProSerTriPlyThirSerSerTyrValGlyAlaSerIle	40	
DB	213	ACATCCATTGCGCACTGCTTCCCAACTGGGGAACGATTCCTATGTTGGGCCAGCAT	272	
QY	41	ValThirAlaValGlyPheSerSerGlyLeuTyrPheGlyCysAlaThrHisSerThGly	60	
DB	273	GTGACGGCGGTGGCTTTCCAAAGGCGCTCGATGAGTGTGCGACACACAGCAGCAGC	332	
QY	61	IleThrGlnCysAspIleTyrSerThirLeuLeuGlyLeuProAlaAspIleGlnAla	80	
DB	333	ATCACCCAGTGGCGATTCACAGAACCTTTTAGACTTCCTGTCGATCCAGCTGCGC	392	
QY	81	GlnAlaMetMetValThirSerSerAlaIleSerSerLeuAlaCysIleIleSerValIle	100	
DB	393	CAGGCCATGATGATGAGAGCTCCAGTGCATATGCTTCGCTGCTTATTAATCTCTGGTG	452	
QY	101	GlyMetArgCysThrValPheCysGlnLeuSerArgAlaIysAspArgValAlaValAla	120	
DB	453	GGCATGAGATGCACGGTCTCTGCCAGAGATTCCTGAGCTAAGACAGAGTGGCTGATGTG	512	
QY	121	GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleAspLeu	140	
DB	513	GGTGGAGTCTTTTTCATCCCTTGGGAGATCTGGGGCTTTATCCAGATGCTGGAACTTT	572	
QY	141	HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle	160	
DB	573	CATGGCATCTCTGGGCACTTCTACTCCCGCTGTTCTTACAGCATGAATTTGAATTT	632	
QY	161	GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle	180	
DB	633	GGAGAGGCTGTGATCTTGGGATCATCTCAGCCCTGTATATCTAATGATGAGCGAGTCATC	692	
QY	181	LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla	200	
DB	693	CTTTGCTTTCTTCCTGCTCGCCCGAGGCAATCGTACCAACTACTATGATGCTTAACAGGCC	752	
QY	201	GlnProLeuAlaThrArg	206	
DB	753	CAGCTTCTTCCACTAGG	770	
RESULT 15				
BE513091		945 bp	mRNA	linear
LOCUS	601117545F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3545171 5',			
DEFINITION	mRNA sequence.			
ACCESSION	BE513091			
VERSION	BE513091.1 GI:9720302			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	EMBL/GenBank/CCDS: Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 945)			
TITLE	NIH-MGC http://mgs.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			

Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LICM241 row: 1 column: 12
 High quality sequence start: 36
 High quality sequence stop: 782.
 Location/Qualifiers

FEATURES
Source

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1..945
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:3545171"
  /issue_type="adenocarcinoma cell line"
  /lab_host="DH10B (phage-resistant)"
  /clone_1b="NIH MGC 15"
  /note="Organ: colon; Vector: POTB; Site 1: XhoI; Site 2:
  EcoRI; cDNA made by oligo-dT priming. Directionally
  cloned into EcoRI/XhoI sites using the following 5'
  adaptor: GGACGAG(G). Size selected >500bp for average
  insert size 1.8kb. Library constructed by Ling Hong in
  the laboratory of Gerald M. Rubin (University of
  California, Berkeley) using ZAP-cDNA synthesis kit
  (Stratagene) and Superscript II RT (Life Technologies)"

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ORIGIN

Alignment Scores:

Pred. No.: 3.96e-98 Length: 945
 Score: 962.50 Matches: 208
 Percent Similarity: 91.38% Conservative: 4
 Best Local Similarity: 89.66% Mismatches: 15
 Query Match: 81.98% Indels: 6
 DB: 2 Gaps: 1

US-09-787-677a-3 (1-230) x BE513091 (1-945)

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QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
DB 187 ATGGCCCTCTTGCGCTCCCACTGTGGCTACATCTTCTGGGGCTTTTGGGC 246
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
DB 247 ACACGTGGTGGCATGCTGCTCCCACTGGAAACAAAGTTTATGTCGGTCCAGCAT 306
QY 41 ValThrAlaValGlyPheSerTyrGlyLeuTyrPheGluCysAlaIleHisSerThrGly 60
DB 307 GTGACACAGTGGCTTCTCCCAAGGCTCTGATGGATGTGCCACACACACAGCAGGC 366
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
DB 367 ATCACCCAGGTGTGACATATAGCACTTCTGGGCTGCGCCGTGACATCCAGCTGCC 426
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 427 CAGGCCATGATGTGACATCCAGTGCATCTCTCCCTGGCTGATTAATCTCTGTG 486
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
DB 487 GGCAATGAGATGCACAGTCTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGTAGCA 546
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrAsnLeu 140
DB 547 GGTGGAGTCTT-TTTCATCTTGGAGGCTCTCTGGGATTCATCTCTGTTGCTGGAAATCTT 605
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLeuPheGlu-I 160
DB 606 CATGGGATCTCAACGGACTTACTACCACTGGTGTGTCACAGCATGAATTTGAAGAT 665
QY 160 egiylualaleuTyrleuglyileileserSerleupheser-leuilealaglylier 180

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DB 666 TGGCAGAGGCTTTTACTTGGGCTTATTTCTTCCCTGTTCTCCCTGATAGCTGAATCA 725
QY 180 le-leuCyapheSerCysSerSerGlnArgAsnArgSerAntTyrTyrAspAlaTyrGln 199
DB 726 TTCTCTGCTTTCCTGCTCATCTCCAGAAATGGGTCCAACTACTACATGCTTACCAA 785
QY 200 -AlaGlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlyValIysSe 219
DB 786 GGGGCCACCTCTTGCACAGAGAGCTCTCCAGGCGTTGGTCACTTCCCAAGGCAAGA-- 843
QY 219 rGluPheAsnSerTyrSerLeuThrGly 228
DB 844 -GTGTTTCATCTTACAGCCTGACAGGG 870

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Search completed: December 20, 2004, 15:38:33
 Job time : 3205 secs